Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**Q9R7I4_HELPY**
Primary accession number	**Q9R7I4**
Secondary accession numbers	None
Integrated into TrEMBL on	May 1, 2000
Sequence was last modified on	May 1, 2000 (Sequence version 1)
Annotations were last modified on	February 7, 2006 (Entry version 16)

Name and origin of the protein

Protein name	**Adhesin-binding fucosylated histo-blood group antigen**
Synonyms	None
Gene name	**Name: babA1**
From	Helicobacter pylori (Campylobacter pylori) [TaxID: 210]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

References

[1] NUCLEOTIDE SEQUENCE.
STRAIN=CCUG 17875;
DOI=10.1126/science.279.5349.373; PubMed=9430586 [NCBI, ExPASy, EBI, Israel, Japan]
Ilver D., Arnqvist A., Ogren J., Frick I.M., Kersulyte D., Incecik E.T., Berg D.E., Covacci A. Engstrand L., Boren T.;
"Helicobacter pylori adhesin binding fucosylated histo-blood group antigens revealed by retagging.";
Science 279:373-377(1998).

WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Wednesday, October 11, 2006

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L1	dgvy	3
☐	L2	aspglyvaltyr	0
☐	L3	asp-gly-val-tyr	0
☐	L4	asp-gly-val-tyr$	0
☐	L5	$asp-gly-val-tyr$	2
☐	L6	$dgvy$	122

END OF SEARCH HISTORY

DERWENT-ACC-NO: 2001-390241
DERWENT-WEEK: 200356

TITLE: Preparation of protein-specific antibodies, useful particularly for detecting haptoglobin for diagnosis of e.g. infection, by immunization with specific protein and its fragment

INVENTOR: HENNIES, M

PATENT-ASSIGNEE: GIESING M (GIESI), HENNIES M (HENNI)

PRIORITY-DATA: 1999DE-1060500 (December 15, 1999)

Search Selected | Search ALL | Clear

PATENT-FAMILY:

	PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
☐	US 20030158391 A1	August 21, 2003		000	C07K016/20
☐	WO 200144299 A2	June 21, 2001	G	026	C07K016/00
☐	DE 19960500 A1	July 12, 2001		000	A61K039/00
☐	EP 1237927 A2	September 11, 2002	G	000	C07K016/00

DESIGNATED-STATES: CA US AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TR

APPLICATION-DATA:

PUB-NO	APPL-DATE	APPL-NO	DESCRIPTOR
US20030158391A1	December 15, 2000	2000WO-EP12798	
US20030158391A1	September 16, 2002	2002US-0148636	
WO 200144299A2	December 15, 2000	2000WO-EP12798	
DE 19960500A1	December 15, 1999	1999DE-1060500	
EP 1237927A2	December 15, 2000	2000EP-0985167	
EP 1237927A2	December 15, 2000	2000WO-EP12798	
EP 1237927A2		WO 200144299	Based on

INT-CL (IPC): A61K 39/00; A61K 39/395; C07K 7/08; C07K 14/47; C07K 16/00; C07K 16/18; C07K 16/20; C07K 16/44; C12P 21/04; C12P 21/08; G01N 33/53; G01N 33/68

ABSTRACTED-PUB-NO: WO 200144299A
BASIC-ABSTRACT:

NOVELTY - Preparation of protein-specific antibodies (Ab) by immunization where the host is treated with an immunization cocktail containing the protein (I) and at least one fragment (II) of (I), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) immunization cocktail containing (I), at least one (II) and optionally auxiliaries;

(2) the peptides VETGSEATDIEDDSSA (III) and SRQFYRLRTEGDGVYTLNSEK (IV);

(3) polyclonal, cross-reactive antiserum, specific for haptoglobin (A) of at least two farm or domestic animals and prepared by the new method; and

(4) immunoassay kit containing at least one antiserum of (3) and additional components.

USE - Ab, particularly as antisera, are especially used for determination of haptoglobin (A), an acute phase protein, in farm and domestic animals, for diagnosis of infection, inflammation, trauma or immunological stress, also for monitoring treatment, in stock management and for optimization of living conditions, or to provide an early indication of successful vaccination.

ADVANTAGE - Ab can detect (A) from several different species with equal sensitivities (known methods are species-specific), particularly less than 1, especially 0.01, mg/ml. They are suitable for analyzing samples that have been stored for a long time (over 2 years at -18 deg. C) or under unfavorable conditions, or those that have been inactivated by heating.

ABSTRACTED-PUB-NO: WO 200144299A
EQUIVALENT-ABSTRACTS:

CHOSEN-DRAWING: Dwg.0/0

DERWENT-CLASS: B04 D16
CPI-CODES: B04-B04L; B04-C01D; B04-C01E; B04-G01; B04-G22; B04-N02; B04-N04A; B11-C07A; B12-K04A; D05-H09; D05-H11B;

Previous Doc Next Doc Go to Doc#

Blast search 10/06 10p

- ☐ tr Q1HW12 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q1HW13 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q6T8D5 _HELPY BabB (BabB2) [Helicobacter pylori (Campylobacter.
- ☐ tr Q8GNW2 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q8GNW1 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q8GNV7 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q7WV99 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q7WV84 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q7WV81 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q5Q1P2 _HELPY BabB/BabA1 fusion protein 1 (Fragment) [babB/bab.
- ☐ tr Q5Q1P1 _HELPY BabB/BabA1 fusion protein 2 (Fragment) [babB/bab.
- ☐ tr Q8GNW0 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q8GNV8 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q8GNV6 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q7WVA4 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q7WVA2 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q7WVA1 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q7WV74 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q7WV69 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q6T8D3 _HELPY BabA [Helicobacter pylori (Campylobacter pylori)]
- ☐ tr O52269 _HELPY Adhesin binding fucosylated histo-blood group an.
- ☐ tr O51811 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q6U2C5 _HELPY Adhesin-binding fucosylated histo-blood group (F.
- ☐ tr Q5G5J5 _HELPY Adhesin-binding fucosylated histo-blood group (F.
- ☐ tr Q17SY9 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ4 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q8GNV9 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q1CSX9 _HELPH Outer membrane protein BabA [HPAG1_0876] [Helico.
- ☐ tr Q17SZ6 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SW3 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SY4 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SY2 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SW9 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SY1 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SV2 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SX6 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SY3 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SY0 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SY8 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ7 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SX4 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SU9 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.

- ☐ tr Q17SX7 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SU3 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SV6 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SV8 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SW6 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SX9 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ2 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SX5 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SV1 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SW0 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SX8 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ3 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SY7 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SU4 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.

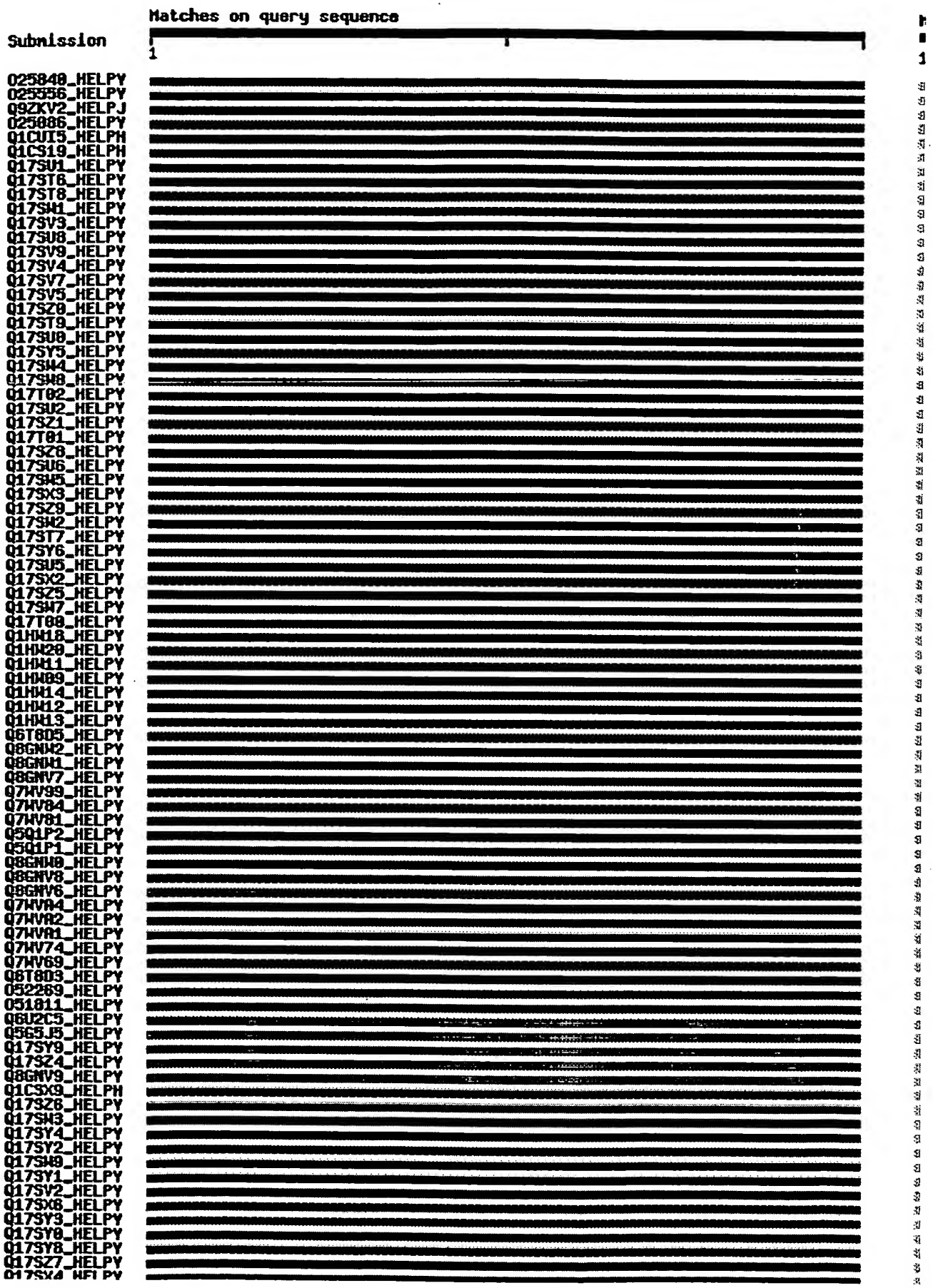
Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits


Matches on query sequence
Submission
1
Q25848_HELPY
O25356_HELPY
Q9ZKV2_HELPJ
O25086_HELPY
Q1CUI5_HELPH
Q1CS19_HELPH
Q17SU1_HELPY
Q17ST6_HELPY
Q17ST8_HELPY
Q17SW1_HELPY
Q17SV3_HELPY
Q17SU8_HELPY
Q17SV9_HELPY
Q17SV4_HELPY
Q17SV7_HELPY
Q17SV5_HELPY
Q17SZ0_HELPY
Q17ST9_HELPY
Q17SU0_HELPY
Q17SY5_HELPY
Q17SW4_HELPY
Q17SW8_HELPY
Q17T02_HELPY
Q17SU2_HELPY
Q17SZ1_HELPY
Q17T01_HELPY
Q17SZ8_HELPY
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Q17SX3_HELPY
Q17SZ9_HELPY
Q17SW2_HELPY
Q17ST7_HELPY
Q17SY6_HELPY
Q17SU5_HELPY
Q17SX2_HELPY
Q17SZ5_HELPY
Q17SW7_HELPY
Q17T00_HELPY
Q1HW18_HELPY
Q1HW20_HELPY
Q1HW11_HELPY
Q1HW09_HELPY
Q1HW14_HELPY
Q1HW12_HELPY
Q1HW13_HELPY
Q6T8D5_HELPY
Q8GNW2_HELPY
Q8GNW1_HELPY
Q8GNV7_HELPY
Q7WV99_HELPY
Q7WV84_HELPY
Q7WV81_HELPY
Q5Q1P2_HELPY
Q5Q1P1_HELPY
Q8GNW0_HELPY
Q8GNV8_HELPY
Q8GNV6_HELPY
Q7WVR4_HELPY
Q7WVR2_HELPY
Q7WVR1_HELPY
Q7WV74_HELPY
Q7WV69_HELPY
Q8T8D3_HELPY
O52269_HELPY
O51811_HELPY
Q6U2C5_HELPY
Q5G5J5_HELPY
Q17SY9_HELPY
Q17SZ4_HELPY
Q8GNV9_HELPY
Q1CSX9_HELPH
Q17SZ6_HELPY
Q17SW3_HELPY
Q17SY4_HELPY
Q17SY2_HELPY
Q17SW9_HELPY
Q17SY1_HELPY
Q17SV2_HELPY
Q17SX8_HELPY
Q17SY3_HELPY
Q17SY0_HELPY
Q17SY8_HELPY
Q17SZ7_HELPY
Q17SX4_HELPY

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17ST8 Q17ST8_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 182 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SW1 Q17SW1_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 241 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SV3 Q17SV3_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 242 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SU8 **BabB (Fragment) [babB] [Helicobacter pylori** 241
Q17SU8_HELPY **(Campylobacter** AA
pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SV9 **BabB (Fragment) [babB] [Helicobacter pylori** 247
Q17SV9_HELPY **(Campylobacter** AA
pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SV4 **BabB (Fragment) [babB] [Helicobacter pylori** 248
Q17SV4_HELPY **(Campylobacter** AA
pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SV7 **BabB (Fragment) [babB] [Helicobacter pylori** 239
Q17SV7_HELPY **(Campylobacter** AA
pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SV5 Q17SV5_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 245 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SZ0 Q17SZ0_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 216 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17ST9 Q17ST9_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 248 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 20 EDDGFYTSVGYQIGEAAQMV 39
```

tr Q17SU0 Q17SU0_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 246 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 20 EDDGFYTSVGYQIGEAAQMV 39
```

tr Q17SY5 Q17SY5_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 222 AA align

```
 Score = 68.1 bits (153), Expect = 4e-11
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SW4 Q17SW4_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 247 AA align

```
 Score = 68.1 bits (153), Expect = 4e-11
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SW8 Q17SW8_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 247 AA align

```
 Score = 68.1 bits (153), Expect = 4e-11
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17T02 Q17T02_HELPY **BabC (Fragment) [babC] [Helicobacter pylori (Campylobacter** 263 AA

pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SU2 Q17SU2_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 244 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17SZ1 Q17SZ1_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 217 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17T01 Q17T01_HELPY **BabC (Fragment) [babC] [Helicobacter pylori (Campylobacter pylori)]** 205 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SZ8 Q17SZ8_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 219 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SU6 Q17SU6_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 143 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SW5 Q17SW5_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 180 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 20 EDDGFYTSVGYQIGEAAQMV 39
```

tr Q17SX3 Q17SX3_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 221 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
```

Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q17SZ9 Q17SZ9_HELPY **BabC (Fragment) [babC] [Helicobacter pylori (Campylobacter pylori)]** 261 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q17SW2 Q17SW2_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 249 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q17ST7 Q17ST7_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 247 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q17SY6 Q17SY6_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 221 AA align

Score = 68.1 bits (153), Expect = 4e-11

Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SU5 Q17SU5_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 241 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 16 EDDGFYTSVGYQIGEAAQMV 35
```

tr Q17SX2 Q17SX2_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 215 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SZ5 Q17SZ5_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 213 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17SW7 **BabB (Fragment) [babB] [Helicobacter pylori** 244

Q17SW7_HELPY **(Campylobacter pylori)]** AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q17T00 **BabC (Fragment) [babC] [Helicobacter pylori** 253
Q17T00_HELPY **(Campylobacter pylori)]** AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q1HW18 **Adhesin-binding fucosylated histo-blood group antigen** 745
Q1HW18_HELPY **[babA]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q1HW20 **Adhesin-binding fucosylated histo-blood group antigen** 744
Q1HW20_HELPY **[babA]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q1HW11 **Adhesin-binding fucosylated histo-blood group antigen** 721
Q1HW11_HELPY **[babA]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q1HW09 **Adhesin-binding fucosylated histo-blood group antigen** 744
Q1HW09_HELPY **[babA]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q1HW14 **Adhesin-binding fucosylated histo-blood group antigen** 736
Q1HW14_HELPY **[babA]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q1HW12 **Adhesin-binding fucosylated histo-blood group antigen** 721
Q1HW12_HELPY **[babA]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
```

Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q1HW13 Q1HW13_HELPY **Adhesin-binding fucosylated histo-blood group antigen [babA] [Helicobacter pylori (Campylobacter pylori)]** 735 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q6T8D5 Q6T8D5_HELPY **BabB (BabB2) [Helicobacter pylori (Campylobacter pylori)]** 706 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37

tr Q8GNW2 Q8GNW2_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 137 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 13 EDDGFYTSVGYQIGEAAQMV 32

tr Q8GNW1 Q8GNW1_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 145 AA align

Score = 68.1 bits (153), Expect = 4e-11

Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 20 EDDGFYTSVGYQIGEAAQMV 39
```

tr Q8GNV7 Q8GNV7_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 135 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 11 EDDGFYTSVGYQIGEAAQMV 30
```

tr Q7WV99 Q7WV99_HELPY **Adhesin-binding fucosylated histo-blood group antigen (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 694 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 11 EDDGFYTSVGYQIGEAAQMV 30
```

tr Q7WV84 Q7WV84_HELPY **Adhesin-binding fucosylated histo-blood group antigen (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 739 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q7WV81 **Adhesin-binding fucosylated histo-blood group antigen** 737

Q7WV81_HELPY **(Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q5Q1P2 Q5Q1P2_HELPY **BabB/BabA1 fusion protein 1 (Fragment) [babB/babA1 fusion] [Helicobacter pylori (Campylobacter pylori)]** 731 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q5Q1P1 Q5Q1P1_HELPY **BabB/BabA1 fusion protein 2 (Fragment) [babB/babA1 fusion] [Helicobacter pylori (Campylobacter pylori)]** 732 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q8GNW0 Q8GNW0_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 135 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 11 EDDGFYTSVGYQIGEAAQMV 30
```

tr Q8GNV8 **BabB (Fragment) [babB] [Helicobacter pylori** 135
Q8GNV8_HELPY **(Campylobacter** AA
pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 11 EDDGFYTSVGYQIGEAAQMV 30
```

tr Q8GNV6 **BabB (Fragment) [babB] [Helicobacter pylori** 135
Q8GNV6_HELPY **(Campylobacter** AA
pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 11 EDDGFYTSVGYQIGEAAQMV 30
```

tr Q7WVA4 **Adhesin-binding fucosylated histo-blood group antigen** 704
Q7WVA4_HELPY **(Fragment)** AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q7WVA2 **Adhesin-binding fucosylated histo-blood group antigen** 695
Q7WVA2_HELPY **(Fragment)** AA
[babB] [Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
```

Sbjct: 12 EDDGFYTSVGYQIGEAAQMV 31

tr Q7WVA1 Q7WVA1_HELPY **Adhesin-binding fucosylated histo-blood group antigen (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 695 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 12 EDDGFYTSVGYQIGEAAQMV 31

tr Q7WV74 Q7WV74_HELPY **Adhesin-binding fucosylated histo-blood group antigen (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 736 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q7WV69 Q7WV69_HELPY **Adhesin-binding fucosylated histo-blood group antigen (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 736 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40

tr Q6T8D3 Q6T8D3_HELPY **BabA [Helicobacter pylori (Campylobacter pylori)]** 742 AA align

Score = 68.1 bits (153), Expect = 4e-11

Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr O52269 **Adhesin binding fucosylated histo-blood group antigen** 741
O52269_HELPY **[babA2]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr O51811 **Adhesin-binding fucosylated histo-blood group antigen** 706
O51811_HELPY **[babB]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 18 EDDGFYTSVGYQIGEAAQMV 37
```

tr Q6U2C5 **Adhesin-binding fucosylated histo-blood group (Fragment)** 134
Q6U2C5_HELPY **[babB]** AA
[Helicobacter pylori (Campylobacter pylori)] align

Score = 65.5 bits (147), Expect = 2e-10
Identities = 19/20 (95%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          E+DGFYTSVGYQIGEAAQMV
Sbjct: 11 ENDGFYTSVGYQIGEAAQMV 30
```

tr Q5G5J5 **Adhesin-binding fucosylated histo-blood group (Fragment)** 138

Q5G5J5_HELPY **[babB] [Helicobacter pylori (Campylobacter pylori)]** AA align

Score = 65.5 bits (147), Expect = 2e-10
Identities = 19/20 (95%), Positives = 20/20 (100%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          E+DGFYTSVGYQIGEAAQMV
Sbjct: 9  ENDGFYTSVGYQIGEAAQMV 28
```

tr Q17SY9 Q17SY9_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 220 AA align

Score = 64.3 bits (144), Expect = 5e-10
Identities = 19/20 (95%), Positives = 19/20 (95%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTS GYQIGEAAQMV
Sbjct: 21 EDDGFYTSAGYQIGEAAQMV 40
```

tr Q17SZ4 Q17SZ4_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 223 AA align

Score = 64.3 bits (144), Expect = 5e-10
Identities = 19/20 (95%), Positives = 19/20 (95%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTS GYQIGEAAQMV
Sbjct: 21 EDDGFYTSAGYQIGEAAQMV 40
```

tr Q8GNV9 Q8GNV9_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 151 AA align

Score = 62.6 bits (140), Expect = 2e-09
Identities = 19/20 (95%), Positives = 19/20 (95%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGY IGEAAQMV
Sbjct: 18 EDDGFYTSVGYXIGEAAQMV 37
```

tr Q1CSX9 Q1CSX9_HELPH **Outer membrane protein BabA [HPAG1_0876] [Helicobacter pylori (strain HPAG1)]** 744 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SZ6 Q17SZ6_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 221 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SW3 Q17SW3_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 247 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

tr Q17SY4 Q17SY4_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 220 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
```

Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40

tr Q17SY2 Q17SY2_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 219 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40

tr Q17SW9 Q17SW9_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 240 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37

tr Q17SY1 Q17SY1_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 221 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40

tr Q17SV2 Q17SV2_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 245 AA align

Score = 59.6 bits (133), Expect = 1e-08

Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

tr Q17SX6 Q17SX6_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 218 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SY3 Q17SY3_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 218 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SY0 Q17SY0_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 136 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SY8 **BabA (Fragment) [babA] [Helicobacter pylori** 210

Q17SY8_HELPY **(Campylobacter pylori)]** AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYXSAGYQIGEAAQMV 37
```

tr Q17SZ7 **BabA (Fragment) [babA] [Helicobacter pylori**
Q17SZ7_HELPY **(Campylobacter pylori)]** 214 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SX4 **BabA (Fragment) [babA] [Helicobacter pylori**
Q17SX4_HELPY **(Campylobacter pylori)]** 220 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SU9 **BabB (Fragment) [babB] [Helicobacter pylori**
Q17SU9_HELPY **(Campylobacter pylori)]** 247 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SX7 **BabA (Fragment) [babA] [Helicobacter pylori** 222
Q17SX7_HELPY **(Campylobacter** AA
pylori)] align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SU3 **BabB (Fragment) [babB] [Helicobacter pylori** 247
Q17SU3_HELPY **(Campylobacter** AA
pylori)] align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

tr Q17SV6 **BabB (Fragment) [babB] [Helicobacter pylori** 244
Q17SV6_HELPY **(Campylobacter** AA
pylori)] align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 20 EDDGFYMSAGYQIGEAAQMV 39
```

tr Q17SV8 **BabB (Fragment) [babB] [Helicobacter pylori** 247
Q17SV8_HELPY **(Campylobacter** AA
pylori)] align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
```

Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37

tr Q17SW6 Q17SW6_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 244 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37

tr Q17SX9 Q17SX9_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 225 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40

tr Q17SZ2 Q17SZ2_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 224 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 1 EDDGFYTSVGYQIGEAAQMV 20
EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40

tr Q17SX5 Q17SX5_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 152 AA align

Score = 59.6 bits (133), Expect = 1e-08

Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

tr Q17SV1 Q17SV1_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 247 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

tr Q17SW0 Q17SW0_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 247 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

tr Q17SX8 Q17SX8_HELPY **BabA (Fragment) [babA] [Helicobacter pylori (Campylobacter pylori)]** 129 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 20 EDDGFYMSAGYQIGEAAQMV 39
```

tr Q17SZ3 **BabA (Fragment) [babA] [Helicobacter pylori** 212

Q17SZ3_HELPY **(Campylobacter pylori)]** AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

tr Q17SY7 **BabA (Fragment) [babA] [Helicobacter pylori**
Q17SY7_HELPY **(Campylobacter pylori)]** 216 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 21 EDDGFYMSAGYQIGEAAQMV 40
```

tr Q17SU4 **BabB (Fragment) [babB] [Helicobacter pylori**
Q17SU4_HELPY **(Campylobacter pylori)]** 245 AA align

Score = 59.6 bits (133), Expect = 1e-08
Identities = 18/20 (90%), Positives = 18/20 (90%)

```
Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFY S GYQIGEAAQMV
Sbjct: 18 EDDGFYMSAGYQIGEAAQMV 37
```

Database: UniProtKB
Posted date: Oct 2, 2006 7:55 PM
Number of letters in database: 996,993,119
Number of sequences in database: 3,006,747

Database: /home/local/blastnet/database/EXPASY////UniProtKB.01
Posted date: Oct 2, 2006 7:57 PM
Number of letters in database: 148,919,217
Number of sequences in database: 487,898

Lambda K H

```
   0.337    0.280     1.75

Gapped
Lambda      K       H
   0.294    0.110    0.610


Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Hits to DB: 12,186,021
Number of Sequences: 3494645
Number of extensions: 36858
Number of successful extensions: 2103
Number of sequences better than 10.0: 100
Number of HSP's better than 10.0 without gapping: 249
Number of HSP's successfully gapped in prelim test: 1
Number of HSP's that attempted gapping in prelim test: 1854
Number of HSP's gapped (non-prelim): 250
length of query: 20
length of database: 1,145,912,336
effective HSP length: 10
effective length of query: 10
effective length of database: 1,110,965,886
effective search space: 11109658860
effective search space used: 11109658860
T: 16
A: 15
X1: 15 ( 7.3 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 41 (21.8 bits)
S2: 64 (30.3 bits)
Wallclock time: 8 seconds
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#18 **Related Articles** for **PubMed** (Select **7559328**)	09:55:38	1(
#14 Search **"outer membrane protein u" helicobacter**	09:43:57	1:
#13 Search **"outer membrane protein u"**	09:43:45	183:
#12 Search **hopu**	09:43:23	
#11 Search **hop-u helicobacter pylori**	09:43:17	
#9 Search **hopu helicobacter pylori**	09:42:45	227
#8 Search **hopu pylori**	09:42:30	239
#7 Search **omp19 pylori**	09:42:17	
#6 Search **omp9 pylori**	09:42:09	
#4 Search **omp-9 pylori**	09:41:23	
#3 Search **omp28 pylori**	09:41:13	
#2 Search **omp29 pylori**	09:40:50	
#1 Search **omp2 pylori**		

```
SYSTEM:OS  - DIALOG OneSearch
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         (c) format only 2006 Dialog
  File   5:Biosis Previews(R) 1969-2006/Oct W1
         (c) 2006 The Thomson Corporation
  File  34:SciSearch(R) Cited Ref Sci 1990-2006/Oct W1
         (c) 2006 The Thomson Corp
  File  35:Dissertation Abs Online 1861-2006/Sep
         (c) 2006 ProQuest Info&Learning
  File  45:EMCare 2006/Oct W1
         (c) 2006 Elsevier B.V.
  File  65:Inside Conferences 1993-2006/Oct 10
         (c) 2006 BLDSC all rts. reserv.
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         (c) 2006 Elsevier B.V.
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  File  91:MANTIS(TM) 1880-2006/Jan
         2001 (c) Action Potential
  File  94:JICST-EPlus 1985-2006/Jul W1
         (c)2006 Japan Science and Tech Corp(JST)
  File  98:General Sci Abs 1984-2006/Oct
         (c) 2006 The HW Wilson Co.
  File 135:NewsRx Weekly Reports 1995-2006/Oct W1
         (c) 2006 NewsRx
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         (c) 2006 INIST/CNRS
  File 149:TGG Health&Wellness DB(SM) 1976-2006/Sep W4
         (c) 2006 The Gale Group
  File 156:ToxFile 1965-2006/Oct W1
         (c) format only 2006 Dialog
  File 159:Cancerlit 1975-2002/Oct
         (c) format only 2002 Dialog
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Please see HELP NEWS159.
  File 162:Global Health 1983-2006/Aug
         (c) 2006 CAB International
  File 164:Allied & Complementary Medicine 1984-2006/Oct
         (c) 2006 BLHCIS
  File 172:EMBASE Alert 2006/Oct 11
         (c) 2006 Elsevier B.V.
  File 266:FEDRIP 2006/Aug
        Comp & dist by NTIS, Intl Copyright All Rights Res
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         (c) 2006 Reed Business Information Ltd.
  File 370:Science 1996-1999/Jul W3
         (c) 1999 AAAS
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information.
  File 399:CA SEARCH(R) 1967-2006/UD=14516
         (c) 2006 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
IPCR/8 classification codes now searchable as IC=. See HELP NEWSIPCR.
  File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
         (c) 2006 The Thomson Corp
  File 444:New England Journal of Med. 1985-2006/Sep W4
         (c) 2006 Mass. Med. Soc.
  File 467:ExtraMED(tm) 2000/Dec
         (c) 2001 Informania Ltd.

      Set  Items  Description
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Cost is in DialUnits
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Terminal set to DLINK
? t s16/9/4 7

Set     Items   Description
S1          2   'HOPU'
S2         81   E3-E6
S3          5   'HOPZ PROTEIN, HELICOBACTER PYLORI'
S4          4   RD  (unique items)
S5      10865   'OMP'
S6         47   'OMP29' OR 'OMP29 PROTEIN, HELICOBACTER PYLORI'
S7        474   'OMP2'
S8          1   'OMP2 OUTER MEMBRANE PROTEIN 2'
S9        155   E13-E20
S10        71   E3-E5
S11        11   'OMP9'
S12        43   'OMP28'
S13       226   (S5 OR S6 OR S7 OR S8 OR S9 OR S10 OR S11 OR S13) (100N) (-
              HELICOB? OR PYLORI OR PYLORIS OR PYLORIDIS OR HPYLORI)
S14       135   RD  (unique items)
S15       121   S14/1997:2006
S16        14   S14 NOT S15
? t s16/3,kwic/11 12 13 14

 16/9/4     (Item 2 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
(c) 2006 The Thomson Corporation. All rts. reserv.

0007539847   BIOSIS NO.: 199141052473
ACTION OF  HELICOBACTER - PYLORI  OUTER MEMBRANE PROTEINS  OMP  ON
  PERIPHERAL BLOOD LYMPHOCYTES
AUTHOR: BROOKS W P (Reprint); HATZ R A; PORTER F R; KRAEMLING H-J
AUTHOR ADDRESS: DEP SURGERY, KLINKUM GROSSHADERN, 8000 MUNICH 70, GERMANY**
  GERMANY
JOURNAL: Gastroenterology  100 (5 PART 2): pA564 1991
CONFERENCE/MEETING: DIGESTIVE DISEASE WEEK AND THE 92ND ANNUAL MEETING OF
THE AMERICAN GASTROENTEROLOGICAL ASSOCIATION, NEW ORLEANS, LOUISIANA, USA,
MAY 19-22, 1991. GASTROENTEROLOGY.
ISSN: 0016-5085
DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH
DESCRIPTORS: ABSTRACT HUMAN WESTERN BLOT ELISA
DESCRIPTORS:
  MAJOR CONCEPTS: Blood and Lymphatics--Transport and Circulation; Cell
    Biology; Clinical Endocrinology--Human Medicine, Medical Sciences;
    Immune System--Chemical Coordination and Homeostasis; Infection;
    Metabolism
  BIOSYSTEMATIC NAMES: Aerobic Helical or Vibrioid Gram-Negatives--
    Eubacteria, Bacteria, Microorganisms; Hominidae--Primates, Mammalia,
    Vertebrata, Chordata, Animalia
  COMMON TAXONOMIC TERMS: Bacteria; Eubacteria; Microorganisms; Animals;
    Chordates; Humans; Mammals; Primates; Vertebrates
CONCEPT CODES:
  00520 General biology - Symposia, transactions and proceedings
  02508 Cytology - Human
  10064 Biochemistry studies - Proteins, peptides and amino acids
  10504 Biophysics - Methods and techniques
  10804 Enzymes - Methods
```

13012 Metabolism - Proteins, peptides and amino acids
15008 Blood - Lymphatic tissue and reticuloendothelial system
34502 Immunology - General and methods
34504 Immunology - Bacterial, viral and fungal
34508 Immunology - Immunopathology, tissue immunology
36002 Medical and clinical microbiology - Bacteriology
BIOSYSTEMATIC CODES:
06210 Aerobic Helical or Vibrioid Gram-Negatives
86215 Hominidae

16/9/7 (Item 1 from file: 65)
DIALOG(R)File 65:Inside Conferences

00270697 INSIDE CONFERENCE ITEM ID: CN002510881
Activation of Granulocytes by H. pylori OMP as a Mechanism for the Pathogenesis of Type B Gastritis
Enders, G.; Von Kan, N.; Brooks, W.; Kraemling, H.-J.
CONFERENCE: 111 Kongress
CHIRURGISCHES FORUM FUR EXPERIMENTELLE UND KLINISCHE FORSCHUNG , 1994; 111th P: 57-62
Springer-Verlag, 1994
ISBN: 3540578463
LANGUAGE: German DOCUMENT TYPE: Conference Papers
CONFERENCE EDITOR(S): Trede, M.; Seifert, J.; Hartel, W.
CONFERENCE SPONSOR: Deutschen Gesellschaft fur Chirurgie
CONFERENCE LOCATION: Munich, Germany
CONFERENCE DATE: Apr 1994 (199404)

BRITISH LIBRARY ITEM LOCATION: 3181.473000
NOTE:
In German or English
DESCRIPTORS: chirurgie
? logoff hold
>>>KWIC option is not available in file(s): 399

16/3,KWIC/11 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

121225957 CA: 121(19)225957j JOURNAL
Siderophore production and iron-regulated envelope proteins of Helicobacter pylori
AUTHOR(S): Illingworth, David Simon; Walter, Kim Suzanne; Griffiths, Phillippa Leigh; Barclay, Raymond
LOCATION: Department Microbiology, University Reading, Reading, UK, RG6 2AJ
JOURNAL: Zentralbl. Bakteriol. DATE: 1993 VOLUME: 280 NUMBER: 1-2
PAGES: 113-19 CODEN: ZEBAE8 ISSN: 0934-8840 LANGUAGE: English

16/3,KWIC/12 (Item 2 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

119067741 CA: 119(7)67741m JOURNAL
Iron acquisition by Helicobacter pylori: Importance of human lactoferrin
AUTHOR(S): Husson, Marie Odile; Legrand, Dominique; Spik, Genevieve; Leclerc, Henri

LOCATION: Lab. Bacteriol. A, Fac. Med., 59045, Lille, Fr.
JOURNAL: Infect. Immun. DATE: 1993 VOLUME: 61 NUMBER: 6 PAGES: 2694-7
CODEN: INFIBR ISSN: 0019-9567 LANGUAGE: English

16/3,KWIC/13 (Item 3 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

115180948 CA: 115(17)180948q JOURNAL
Characterization of an immunoreactive species-specific 19-kilodalton outer membrane protein from Helicobacter pylori by using a monoclonal antibody
AUTHOR(S): Drouet, Emmanuel B.; Denoyel, Gerard A.; Boude, Monique; Wallano, Eyob; Andujar, Mauricio; De Montclos, Henri P.
LOCATION: Cent. Ultrastruct. Pathol., Inst. Pasteur de Lyon, 69007, Lyons, Fr.
JOURNAL: J. Clin. Microbiol. DATE: 1991 VOLUME: 29 NUMBER: 8 PAGES: 1620-4 CODEN: JCMIDW ISSN: 0095-1137 LANGUAGE: English

16/3,KWIC/14 (Item 4 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

115156568 CA: 115(15)156568v JOURNAL
Oral immunization against Helicobacter pylori
AUTHOR(S): Czinn, Steven J.; Nedrud, John G.
LOCATION: Dep. Pediatr., Case West. Reserve Univ., Cleveland, OH, 44106, USA
JOURNAL: Infect. Immun. DATE: 1991 VOLUME: 59 NUMBER: 7 PAGES: 2359-63 CODEN: INFIBR ISSN: 0019-9567 LANGUAGE: English
?

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     $2.30 Estimated cost File5
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     $0.07 Estimated cost File35
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 $0.26  TELNET
$17.78  Estimated cost this search
$17.78  Estimated total session cost   0.443 DialUnits


Logoff: level 05.12.03 D  09:04:09

You are now logged off
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WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Wednesday, October 11, 2006

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR	
☐	L1	$lectin or lectin$	75409
☐	L2	L1 near10 (helicob$ or pylori or pylroi or pylor or hpylori or h-pylori or pyloris or pyloridis)	34

END OF SEARCH HISTORY

#23	Search **wadstrom lectins bacterial**	15:04:56
#22	Search **nakazawa 1989 pylori**	15:03:32
#19	Search **falk 1994 receptors**	13:56:00
#18	**Related Articles** for **PubMed** (Select **7559328**)	09:55:38
#14	Search **"outer membrane protein u" helicobacter**	09:43:57
#13	Search **"outer membrane protein u"**	09:43:45
#12	Search **hopu**	09:43:23
#11	Search **hop-u helicobacter pylori**	09:43:17
#9	Search **hopu helicobacter pylori**	09:42:45
#8	Search **hopu pylori**	09:42:30
#7	Search **omp19 pylori**	09:42:17
#6	Search **omp9 pylori**	09:42:09
#4	Search **omp-9 pylori**	09:41:23
#3	Search **omp28 pylori**	09:41:13
#2	Search **omp29 pylori**	09:40:50
#1	Search **omp2 pylori**	

Reconsidered search notes DEB

the gastrointestinal tract (24). The Lewis b mouse can be useful for the evaluation of the role of the BabA adhesin as a colonisation/virulence factor and in addition for the evaluation of BabA as a vaccine candidate against acid peptic disease and gastric adenocarcinoma.

In the present study the ReTagging technique was used for the purification of the adhesin part of the microbial receptor-ligand interaction. By the use of purified adhesin/lectin-protein, the ReTagging technique could, in addition, be used to further study the receptor part of the interaction. Identification of the biologically active receptor structure, carrying Le^b oligosaccharides, would aid in the understanding of the mechanisms supporting the chronic *H. pylori* infection.

Inhibition of *H. pylori* binding to ^{125}I-labeled Lewis b antigen by preparations is presented graphically, as a function of antibody concentration (mg/ml) in Fig. 6: 1 ml aliquots of *H. pylori* bacteria (A_{600}= OD 0.10) were pre-incubated with dilution series of antibody preparations, in 0.01-10 mg/ml for 2 hours in phosphate buffered saline (PBS), 0.5 % albumin, 0.05 % Tween-20. Then 500 ng of ^{125}I-labeled conjugate (i.e. an excess of receptor structure) was added and incubated for 30 minutes. After centrifugation, ^{125}I-activity in the bacterial pellet was measured by gamma scintillation counting. The Lewis b blood group antigen glycoconjugates used, i.e. semi-synthetic glycoproteins constructed by the conjugation of purified fucosylated oligosaccharides to serum albumin were from IsoSep AB, Tullinge, Sweden.

Western blot detection of the BabA adhesin by the different antibody preparations is presented in Fig. 7: Molecular weight rainbow marker (2 μL) from Amersham, Buckinghamshire, England, was dissolved in SDS sample buffer (lane 1). Approx. 100 ng of purified BabA adhesin (approx. 74 kDa with degradation product of approx. 55 kDa) was dissolved in SDS sample buffer (lane 2). SDS solubilized protein extracts of strain CCUG 17875 were prepared by dissolving the bacterial pellet corresponding to 0.15 ml of bacteria (A_{600}= OD 0.10) by SDS sample buffer (lane 3). The 3 protein samples were then boiled at 100°C for 5 minutes. The proteins were separated on SDS-PAGE, and transferred to a PVDF-membrane for Western blot immuno analysis. Five sets of PVDF-membranes were prepared. The PVDF membranes were blocked/incubated overnight with 4% human sera/plasma, in phosphate buffered saline, from a patient with no H. pylori infection, i.e. with no serum antibodies against H. pylori. The membrane was then washed in phosphate buffered saline (PBS), 0.5 % albumin, 0.05

1: Immunobiology. 1996 Jul;195(2):199-208. Links

The proliferation of human T lymphocytes stimulated by Helicobacter pylori antigens.

Chmiela M, Paziak-Domanska B, Ljungh A, Wadstrom T, Rudnicka W.

Department of Medical Microbiology, Lund University, Sweden.

Fractionated mononuclear cells (MNCs) were obtained from peripheral blood of healthy human volunteers, seronegative for H. pylori antibodies. The MNCs were stimulated in culture with whole live or heat-killed H. pylori cells or with bacterial cell surface (SA) or cytoplasmic (CA) antigens. There was a marked proliferative response of T cells in cultures stimulated with 10(5) cells/well of live H. pylori, 5 micrograms/well of CA or 5-20 micrograms/well of SA. However, no proliferation was observed in MNC cultures containing higher "doses" of live H. pylori organisms (10(7)/well) or CA (20 micrograms/well). Moreover, higher "doses" of the bacteria or CA entirely inhibited the response of T cells to PHA.

PMID: 8877396 [PubMed - indexed for MEDLINE]

An in vitro Adherence Assay Reveals that Helicobacter pylori Exhibits Cell Lineage-Specific Tropism in the Human Gastric Epithelium

P Falk, KA Roth, T Boren, TU Westblom, JI Gordon, and S Normark

PNAS 1993;90;2035-2039
doi:10.1073/pnas.90.5.2035

Proc. Natl. Acad. Sci. USA
Vol. 90, pp. 2035–2039, March 1993
Microbiology

An *in vitro* adherence assay reveals that *Helicobacter pylori* exhibits cell lineage-specific tropism in the human gastric epithelium

(host–microbial interactions/adhesins/glycoproteins/gastric epithelial cell biology)

PER FALK*†, KEVIN A. ROTH†‡, THOMAS BORÉN*, T. ULF WESTBLOM§, JEFFREY I. GORDON†, AND STAFFAN NORMARK*¶

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ABSTRACT *Helicobacter pylori* is a microaerophilic bacterium found in the stomach of asymptomatic humans as well as patients with acid peptic disease and gastric adenocarcinoma. We have developed an *in situ* adherence assay to examine the cell lineage-specific nature of binding of this organism and to characterize the nature of cell surface receptors that recognize its adhesin. Fluorescein isothiocyanate-labeled *H. pylori* strains were bound to surface mucous cells present in the pit region of human and rat gastric units but not to mucous neck, parietal, or chief cell lineages present in the glandular domains of these units. Binding was abolished by proteinase K treatment of tissue sections and by pretreatment of the bacteria with bovine submaxillary gland mucin, a rich source of fucosylated and sialylated carbohydrates. Several lines of evidence suggest that binding to surface mucous cells is not dependent upon terminal nonsubstituted α2,3- and α2,6-linked sialic acids in the adhesin receptor: (*i*) binding was not inhibited by incubating *H. pylori* strains with sialylated glycoconjugates such as fetuin and free sialyllactose; (*ii*) immunohistochemical stainings using the sialic acid-specific *Sambucus nigra* and *Maackia amurensis* lectins and the cholera toxin B subunit did not detect any sialylated glycoconjugates in these epithelial cells; and (*iii*) binding was not sensitive to metaperiodate under conditions that selectively cleaved carbons 8 and 9 of terminal nonmodified sialic acids. A role for fucosylated epitopes in the glycoprotein(s) that mediate binding of *H. pylori* to surface mucous cells was suggested by the facts that this lineage coexpresses the adhesin receptor and major fucosylated histo-blood group antigens, that monoclonal antibodies specific for histo-blood group antigens H, B, and Le^b block binding, and that the lectin *Ulex europaeus* type 1 agglutinin, which is specific for α-L-fucose, also bound to the same cells that bound the bacteria. Furthermore, human colostrum secretory IgA inhibited adhesion in a metaperiodate- and α-L-fucosidase-sensitive but neuraminidase-independent fashion. The *in situ* adherence assay should be useful in further characterizing the *H. pylori* adhesin and its receptor and for identifying therapeutically useful compounds that inhibit strain-specific and cell lineage-specific binding of this human pathogen.

Helicobacter pylori is a spiral-shaped organism originally assigned to the genus *Campylobacter* (1). This genetically diverse species (2) has been estimated to infect the gastric mucosa of >60% of adult humans by the time they enter their seventh decade (3). Moreover, *H. pylori* has been implicated as a causative agent in chronic active (type B) gastritis (4), gastric and duodenal ulcers (5), and gastric adenocarcinoma (6). A large number of questions remain unanswered about how this organism contributes to these pathogenic states: assessments of cell lineage-specific patterns of binding in the stomach have not been reported, nor is the molecular basis of *H. pylori*'s tropism for the gut understood.

Electron microscopic analyses have shown that the bacteria can adhere to apical membranes of epithelial cells via small cellular projections (adherence pedestals; ref. 7). Studies in model systems such as mouse adrenal Y-1 cells (8) have suggested that surface-associated flexible fibrillar structures that surround this organism function as adhesins or colonization factor antigens to mediate *H. pylori* binding to cellular sialic acid-containing glycoproteins. Binding is inhibited by neuraminidase and fetuin. The organism also produces sialic acid-specific hemagglutinins (9). Moreover, *H. pylori* are able to bind *in vitro* to certain of the acid glycosphingolipids extracted from human stomach such as the ganglioside GM3 (NeuAcα2-3Galβ1-4Glcβ1-1Cer) and sulfatide (SO_3-Galβ1-1Cer) (10). In contrast, *H. pylori* adhesion to HeLa cells appears to be independent of sialyllactose (11).

Cell lineage relationships in the gastric epithelium are not well defined. The best understood system is in the adult mouse where complex regional differences in cell types occur along the cephalocaudal axis of the stomach (12–15). The proximal third (forestomach) is lined with a keratinized stratified epithelium, whereas the distal two-thirds contains a glandular epithelium composed of gastric units. All gastric units contain an upper pit region lined with mucus-producing surface epithelial cells. The midportion of the gastric unit (its isthmus) is composed of proliferating and nonproliferating immature cells (13). The lower portion (gland) of these units may contain intrinsic factor- and pepsinogen-producing chief cells, acid-producing parietal cells, mucous neck cells, and various enteroendocrine cell types (zymogenic glands). They may lack chief and parietal cells and be composed primarily of mucous cells that are distinct from surface mucous cells and several enteroendocrine cell subpopulations (pure mucous glands). The cellular composition of gastric units varies as a function of their location along the cephalocaudal axis (12): zymogenic glands are located in the midportion of the stomach, whereas pure mucous glands are situated in the gastric antrum. The results of [^{3}H]thymidine labeling and electron microscopic studies of mouse gastric units have led Lee and LeBlond (13) to propose that the isthmus region contains stem cells that give rise to daughters, which undergo a bipolar, migration-dependent differentiation. Surface mucous cells migrate up the pit to the luminal surface and have a life-span of ≈3 days (14). The other cell types are thought to arise during their descent to the glands, where the differ-

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Abbreviations: FITC, fluorescein isothiocyanate; DIG, digoxigenin; UEA1, *Ulex europaeus* type 1 agglutinin; SNA, *Sambucus nigra* agglutinin; MAA, *Maackia amurensis* agglutinin.

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entiated members of some lineages have a life-span of >60 days (15).

We have developed an *in situ* assay for *H. pylori* adherence that has allowed us to define host species-specific, gastric epithelial cell lineage-specific, and bacterial strain-specific differences in attachment. In addition, a series of biochemical studies suggest that *H. pylori* adhesins interact with glycoprotein receptor(s) present in the gut epithelium and that this interaction does not require sialylated carbohydrate epitopes.

MATERIALS AND METHODS

***In Situ* Adherence Assay for *H. pylori*.** Multiple samples of adult human esophagus, stomach, duodenum, colon, kidney, cervix, endometrium, and midbrain were obtained from the surgical pathology and autopsy files of the Department of Pathology at Washington University. Only samples of nondiseased tissues were used in these experiments. The gastrointestinal tracts of 250-g Sprague–Dawley rats and 6- to 12-week-old FVB/N mice (16) were removed after sacrifice by cervical dislocation and regionally dissected as described (17). All tissues were fixed in 10% formalin or in a solution of picric acid/formaldehyde/glacial acetic acid (15:5:1; Bouin's fluid) and subsequently embedded in paraffin (17). Five-micron sections were prepared and used for hematoxylin/eosin staining (to identify the cell types present in gastric units and to verify that the tissue samples had no pathologic changes) and/or for subsequent adherence, histochemical, and/or immunocytochemical assays.

Five previously characterized clinical isolates of *H. pylori* were used. NCTC 11637 and 11638 were isolated in 1982 from patients with active chronic gastritis (18). Strain WV229 was from a patient with gastric ulcer, whereas P466 (kindly provided by R. Gilman, The Johns Hopkins University School of Medicine, Baltimore) was obtained from a patient with acute gastritis. Strain MO19 was from an asymptomatic carrier. Strains were grown at 37°C on *Brucella* agar supplemented with 10% bovine blood and 1% IsoVitalex (Becton Dickinson) under microaerophilic conditions (5% O_2/10% CO_2/85% N_2) and 98% humidity. Five days after inoculation, 1 μl of bacteria removed with a sterile loop from a plate was resuspended in 1 ml of 0.15 M NaCl/0.1 M sodium carbonate, pH 9.0 (19), by gentle pipetting. Ten microliters of a 10 mg/ml solution of fluorescein isothiocyanate (FITC, Sigma), freshly prepared in dimethyl sulfoxide, was added to the suspension, which was then incubated for 1 hr at room temperature in the dark. The bacteria were recovered by centrifugation at 3000 × *g* for 5 min, resuspended by gentle pipetting in 1 ml of phosphate-buffered saline (PBS)/0.05% Tween 20, and pelleted by centrifugation as above. The wash cycle was repeated three times. The intensity of FITC labeling of all bacterial strains was similar as judged by inspection of comparable numbers of organisms by fluorescence microscopy. Aliquots (100 μl) were taken from the final suspensions and utilized immediately or stored at −20°C until further use. No differences in attachment patterns were observed between strains labeled and used fresh and strains that were frozen and thawed once before use.

Tissue sections were deparaffinized in xylene and isopropanol, rinsed in water followed by PBS, and then incubated for 15–30 min in blocking buffer (0.2% bovine serum albumin/0.05% Tween 20, prepared in PBS). The FITC-labeled bacterial suspension was diluted 20-fold in blocking buffer and 200 μl was placed on the slide, which was then incubated for 1 hr at room temperature in a humidified chamber. Slides were subsequently washed four to six times with PBS prior to inspection.

To analyze the ability of glycoproteins or free oligosaccharides to block binding, 200-μl suspensions of FITC-labeled bacteria were preincubated for 2 hr at room temperature with the following compounds: bovine submaxillary mucin (Sigma, 500 μg/ml), fetuin (Sigma, 100 μg/ml), asialofetuin (Sigma, 100 μg/ml), human sialyllactose (Sigma, 5 μg/ml), bovine sialyllactose (Sigma, 5 μg/ml), human serum IgA (Cappel Laboratories; 500 μg/ml), and human colostrum secretory IgA (Cappel Laboratories, 15 μg/ml). Bacteria were washed once in blocking buffer before the mixture was added to tissue sections. To further characterize the receptor active domain of human colostrum secretory IgA, periodate oxidation was performed according to a protocol provided in the Glycan detection kit (Boehringer Mannheim). The IgA fraction was then washed with PBS using M_r 10,000 cutoff Centricon filters (Amicon). Human colostrum IgA was also incubated for 2 hr at 37°C with 100 milliunits of bovine kidney α-L-fucosidase or *Vibrio cholerae* neuraminidase (Boehringer Mannheim) prior to incubation with bacteria.

Two other experiments were conducted to ascertain the nature of the bacterial receptor in tissue sections. (*i*) Deparaffinized sections were treated for 2 hr at 37°C with 200 milliunits of proteinase K from *Trichiratum albus* (Boehringer Mannheim). They were subsequently washed three times in PBS, treated with blocking buffer, and overlaid with a suspension of FITC-labeled *H. pylori* strain P466 or WV229. (*ii*) Deparaffinized sections were treated with 10 mM sodium metaperiodate/50 mM sodium acetate, pH 5.5, for 10 min at 0°C to selectively cleave carbons 8 and 9 of the unsubstituted side chain of terminal sialic acids (20) or with 10 mM sodium metaperiodate/50 mM sodium acetate, pH 4.5, for 1 hr at room temperature to cleave carbon–carbon bonds between vicinal hydroxyl groups in (most) carbohydrates with a free carbon in the 3 position (21). Control sections were incubated with 50 mM sodium acetate buffer alone. After two PBS washes, the sections were reduced by adding 50 mM sodium borohydride prepared in PBS (pH 7.6). Following three washes with PBS, suspensions of FITC-labeled strain WV229, P466, or MO19 were applied and the slides were processed as described above. Control experiments were used to establish that under the "harsher" oxidation conditions, the antigenicity of proteins present in gastric epithelial cell lineages was preserved: periodate-treated sections of rat stomach were incubated with a rabbit polyclonal antiserum raised against intrinsic factor and the antigen–antibody complexes were subsequently detected by Texas red-conjugated donkey anti-rabbit IgG (22, 23). The intensity of staining of chief cells was retained in periodate-treated sections, whereas the binding of the α-L-fucose-specific *Ulex europaeus* type 1 lectin (UEA1) to surface mucous cells was completely abolished under the same conditions.

Immunohistochemical Studies. The cellular distribution of sialylated oligosaccharides was examined in human stomach by incubating sections with the following lectins: (*i*) fluorescein-, rhodamine- (List Biological Laboratories, Campbell, CA), or peroxidase- (Sigma) conjugated cholera toxin B subunit (5 μg/ml) (24); (*ii*) digoxigenin (DIG)-conjugated *Sambucus nigra* lectin (SNA, 10 μg/ml, Boehringer Mannheim) (25); and (*iii*) DIG-conjugated *Maackia amurensis* lectin (MAA) (10 μg/ml, Boehringer Mannheim) (26). DIG-conjugated lectins were detected with peroxidase-conjugated monoclonal mouse anti-DIG antibody (500 milliunits of peroxidase per ml, Boehringer Mannheim).

Fucosylated blood group antigens were detected with mouse monoclonal antibodies directed against the histo-blood group antigens A, B, and H (final concentrations = 1 μg of protein per ml; Dakopatts, Glostrup, Denmark) or Le^a and Le^b (10 μg/ml; Immucor, Norcross, GA). Antigen–antibody complexes were visualized with fluorescein- or rhodamine-conjugated rabbit anti-mouse immunoglobulins (30 μg/ml; Dakopatts). The distribution of fucosylated gly-

coconjugates was also assessed by FITC-conjugated UEA1 (5 μg/ml; Sigma).

RESULTS AND DISCUSSION

Analysis of Cell Lineage-Specific Binding of *H. pylori* Using an *in Situ* Adherence Assay. Five clinical isolates of *H. pylori* were labeled with FITC following 5 days of growth on rich media under microaerophilic conditions and then overlaid on sections of formalin-fixed human stomach. Strains NCTC 11637, NCTC 11638, WV229, and P466, all recovered from patients with dyspeptic syndrome, bound to surface mucous cells situated in the upper pit and luminal surface (Fig. 1 *A* and *B*). Mucous neck cells located in the upper portions of the glandular segment of gastric units were negative, indicating that these bacteria were able to distinguish between two differentiated mucus-producing cell lineages present in the stomach (27). No binding to parietal or chief cells was noted in zymogenic glands. Strain MO19, the only isolate tested that was recovered from an asymptomatic "healthy" carrier, did not bind at detectable levels to any human gastric epithelial cell lineage (Fig. 1*C*).

Strains WV229 and P466 did not adhere to the squamous epithelium of human esophagus but did adhere under the reaction conditions employed to esophageal submucosal glands and their ducts and to duodenal villus-associated enterocytes (Fig. 1*D*). We also observed weak binding to enterocytes situated in the colonic homolog of small intestinal villi—the surface epithelial cell cuff that surrounds each crypt orifice (Fig. 1*E*). The intensity of staining (i.e., density of adherent organisms) was considerably less throughout the cephalocaudal axis of the intestine than it was in the stomach epithelium.

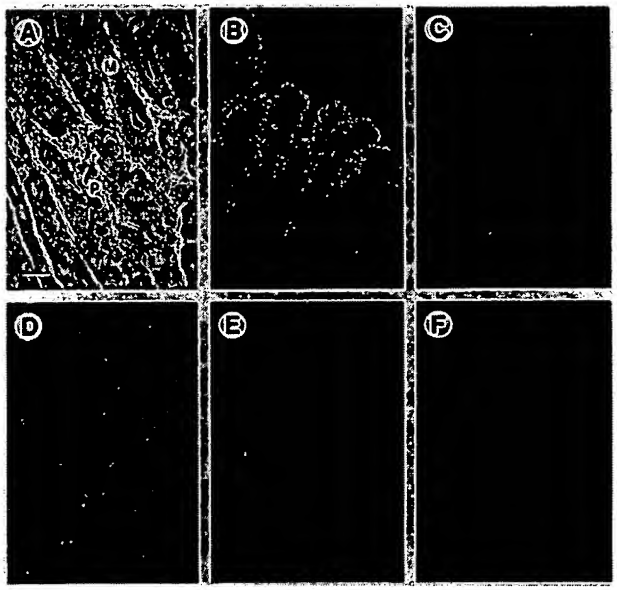

FIG. 1. *In situ* assay for binding of *H. pylori* to gut epithelial cell lineages. (*A*) Section of human stomach stained with hematoxylin/eosin showing the uppermost portion of gastric units in the zymogenic zone. Surface mucous (M) and parietal (P) cells are indicated. (*B* and *C*) Sections of human adult stomach incubated with FITC-labeled *H. pylori* strains WV229 (*B*) and MO19 (*C*). Strain WV229 is associated with surface mucous cells located in the upper pit of gastric units and their associated luminal surfaces. Strain MO19 is not bound to any cell lineage. (*D* and *E*) Incubation of strain WV229 with sections of adult human duodenum (*D*) and colon (*E*). FITC-labeled bacteria stain villus-associated epithelial cells (including enterocytes). Colonocytes located in the upper portion of colonic crypts and their surface epithelial cuffs are very weakly stained. Incubation of sections of human stomach, intestine, and colon with strains NCTC 11637, NCTC 11638, and P466 produced results comparable to those shown in *B*, *D*, and *E* (data not shown). (*F*) Section from the zymogenic zone of an adult Sprague–Dawley rat stomach incubated with strain WV229. Note that although the staining is much weaker than that in the human stomach, this strain of *H. pylori* is associated with surface mucous cells but not with cell lineages associated with the isthmus or glandular domains of rat gastric units. (Bar = 50 μm.)

Control experiments indicated that *H. pylori* P466 and WV229 did not bind to any epithelial cell populations represented in kidney, cervix, or endometrium. Surveys of the central nervous system including the midbrain also failed to produce a signal above background (data not shown).

The *in situ* adherence assay was used next to ascertain whether the cell lineage-specific and *H. pylori* strain-specific patterns of binding occurred in other mammalian species. Strains WV229, P466, and MO19 were incubated with sections of stomach, small intestine, and colon from adult Sprague–Dawley rats and FVB/N mice and stomach from dogs. Strain MO19 was not bound in detectable amounts to tissue sections prepared from any of these three species (data not shown). As in the human stomach, strains WV229 and P466 bound to surface mucous cells in the rat but not to any other differentiated epithelial cell population located in the zymogenic or pure mucous zones (Fig. 1*F*). The intensity of binding was significantly weaker than that observed with human gastric surface mucous cells (compare Fig. 1 *B* and *F*). Unlike in human sections, bacteria adhered to the stratified squamous epithelium of the rat esophagus and forestomach, whereas the small intestinal epithelium was negative with the exception of Brunner's glands (data not shown). The forestomach of the mouse was decorated with adherent bacteria, whereas the remainder of the stomach (i.e., its zymogenic, mucoparietal, and pure mucous zones; ref. 12) and the epithelial and mesenchymal components of the intestine did not yield a signal with FITC-labeled strains WV229 and P466. Finally, no binding of either of the two strains was observed in dog stomach (data not shown).

Biochemical Studies of the Interaction Between *H. pylori* and Gastric Epithelial Cell Lineages. To characterize the nature of the interactions between *H. pylori* and the surface mucous cells, we initially tested the ability of a series of compounds to inhibit binding of FITC-labeled strains P466 and WV229 to sections of human stomach (and proximal small intestine). When calf serum fetuin (a glycoprotein rich in sialylated oligosaccharides including sialyllactose, ref. 28), asialofetuin, soluble sialyllactose prepared from bovine milk (85% NeuAcα2,3Galβ1,4Glc and 15% NeuAcα2,6Galβ1,4Glc), and human milk sialyllactose (15% NeuAcα2,3 and 85% NeuAcα2,6) were preincubated with these two strains, no subsequent reduction in adherence was noted (data not shown). These findings are in agreement with the work of Fauchère and Blaser (11), who observed sialyllactose-independent attachment of *H. pylori* to HeLa cells. However, preincubation of the bacteria with 0.5% bovine submaxillary gland mucin, a rich source of fucosylated and sialylated carbohydrates (29), completely inhibited binding of bacteria to surface mucous cells (Fig. 2 *A* and *B*) and to duodenal, villus-associated, epithelial cells. Human colostrum secretory IgA was also a potent inhibitor: 15 μg/ml (≈40 nM) fully blocked adherence. This glycoprotein carries a highly varied set of N- and O-linked oligosaccharides (30) and has been reported to "nonspecifically" protect gut mucosa against environmental antigens (31). Several observations suggested that this inhibition of *H. pylori* binding by human colostrum secretory IgA was not due to a protein A–Fc receptor-like interaction (32): (*i*) inhibition was abolished by pretreating the secretory IgA with metaperiodate, (*ii*) preincubation at 85°C for 30 min did not affect its inhibitory activity, and (*iii*) α-L-fucosidase treatment of the IgA fraction markedly reduced blocking activity, whereas neuraminidase treatment

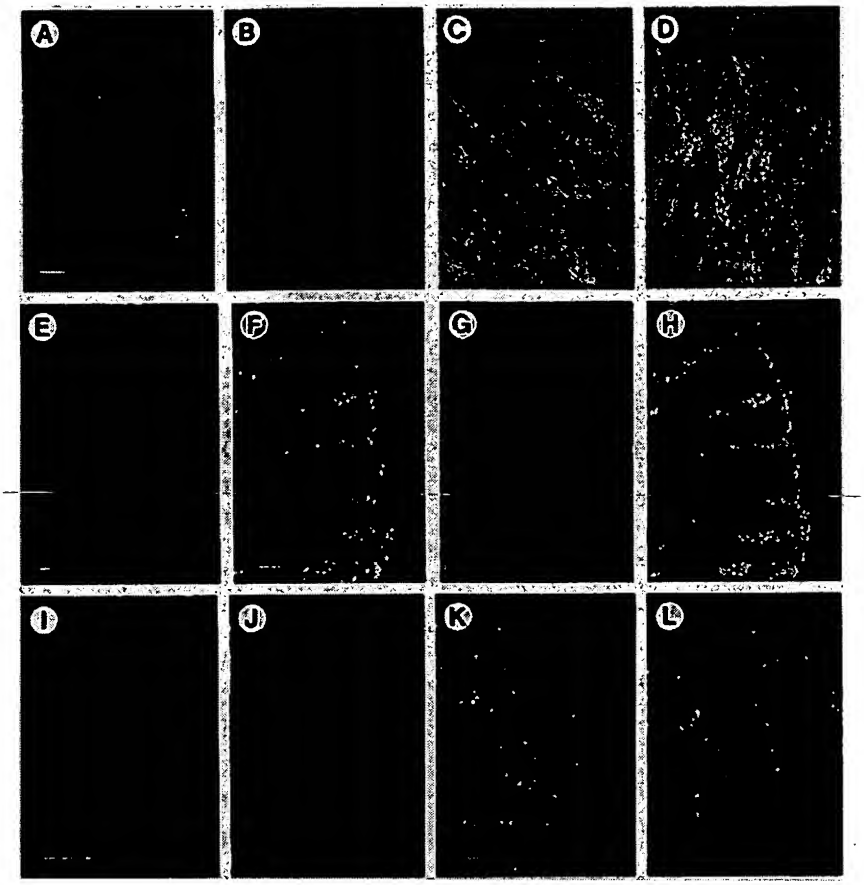

FIG. 2. Characterization of a putative *H. pylori* adhesin receptor as a glycoprotein that lacks sialyllactose. (*A* and *B*) Sections of human stomach containing gastric units with zymogenic glands were incubated with FITC-labeled *H. pylori* strain WV229 (*A*) or with bacteria that had been treated with a 0.5% solution of bovine submaxillary gland mucin (*B*). The mucin preparation produces marked reductions in binding. (*C* and *D*) Sections of human stomach were incubated with DIG-labeled MAA (*C*) or SNA (*D*). DIG-conjugated lectins were detected with a peroxidase-conjugated monoclonal mouse anti-DIG antibody. Note that none of the epithelial cell lineages produced a signal above background when incubated with these lectins that recognize sialic acid-containing carbohydrate epitopes. Control experiments employing the monoclonal antibody alone produced no staining (data not shown). (*E*) Adjacent section of human stomach incubated with rhodamine-conjugated cholera toxin B subunit. Mucus-producing cells located in the isthmus or upper portion of the glandular domain of gastric units react with this lectin. The B subunit does not bind to surface mucous cells located in the pit. (*F–H*) Sections of human stomach were incubated with FITC-labeled *H. pylori* strain P466 (*F*) and a mouse monoclonal antibody directed against the fucosylated blood group antigen H (visualized with rhodamine-conjugated rabbit anti-mouse IgG in *G*). (*H*) Double exposure showing that surface mucous cells coexpress the bacterial adhesin receptor and the blood group antigen. Note the reduction in adherence of bacteria to surface mucous cells (*F*) when compared to sections not treated with this monoclonal antibody (e.g., *A*). Similar reductions in binding were obtained using mouse monoclonal antibodies directed against fucosylated blood group antigens B and Le^b (data not shown). Nonimmune mouse IgG failed to produce this effect (data not shown). (*I*) Section of human stomach was incubated with FITC-conjugated UEA1. The lectin binds to surface mucous cells. (*J*) Pretreatment of a section of human stomach with sodium metaperiodate (pH 5.5) at 0°C for 10 min produces no appreciable reduction in binding of UEA1. (*K* and *L*) The binding of *H. pylori* to surface and pit mucous cells (*K*) was also unaffected by the sodium metaperiodate pretreatment (*L*). (Bars = 50 μm.)

had no detectable effect. In comparison, human serum IgA did not inhibit binding at concentrations as high as 4.5 μM (data not shown). Pretreatment of sections of human stomach with proteinase K also produced marked decrease in the binding of the two *H. pylori* strains (data not shown). Together, these results raised the possibility that binding is mediated by a fucosylated rather than a sialylated glycoprotein receptor expressed on surface mucous cells.

The suggestion that binding of *H. pylori* adhesin(s) to the surface mucous cell population of human stomach does not depend on sialic acid epitopes in a cellular receptor is supported by the results of two additional experiments. First, the distribution of sialic acid-containing complex carbohydrates in the human gastric mucosa does not correlate with the bacterial patterns of adherence. MAA is specific for NeuAcα2,3Galβ1,4GlcNAc epitopes (26), whereas *S. nigra* agglutinin recognizes NeuAcα2,6Gal/GalNAc structures (25). Binding of the MAA and SNA lectins was confined to the submucosal compartment of the human stomach: they did not react with members of any gastric epithelial cell lineage (Fig. 2 *C* and *D*). The cholera toxin B subunit recognizes sialic acid linked to internally positioned galactose—i.e., GalNAcβ1,4(NeuAcα2,3)Gal-β (24). This lectin did not bind to surface mucous cells but rather was confined to mucous neck cells located in the upper glandular domains of gastric units (Fig. 2*E*). Control experiments demonstrated (*i*) MAA binding to surface mucous cells in the dog stomach, (*ii*) binding of SNA to surface mucous and parietal cells, and (*iii*) no binding of cholera toxin B subunit to any gastric epithelial cell lineage in this species (data not shown), suggesting that these lectins can be used to define fundamental differences in the differentiation program of the surface mucous cell lineage between dog and human—differences that may account for their distinct abilities to bind *H. pylori*. Second, when tissue sections were incubated with 10 mM metaperiodate/sodium acetate, pH 5.5, at 0°C (20), selective loss of SNA binding to surface mucous cells in dog stomach was seen (data not shown). Using these periodate oxidation conditions, we found that there was no reduction in adherence of any of the binding strains to human stomach or small intestinal epithelial populations compared to control sections that had been treated with the sodium acetate buffer alone (data not shown).

Other observations support a role for fucosylated epitopes in the glycoprotein(s) that mediate binding of *H. pylori* to surface mucous epithelial cells in the human stomach. The receptor sites for FITC-labeled strains P466 and WV229 are coexpressed in members of this epithelial cell lineage together with the fucosylated histo-blood group antigens H, B, and Le^b (e.g., see Fig. 2 *F–H*). Moreover, bacterial binding was reduced in sections that had been preincubated with monoclonal antibodies specific for either of the three blood group antigens (e.g., see Fig. 2 *F–H*). UEA1, which is specific for α-L-fucose, also bound to the same cells that contained *H. pylori* receptors (Fig. 2*I*). The metaperiodate oxidation reaction conditions employed above had no effect on UEA1 binding (Fig. 2*J*) or on *H. pylori* binding (Fig. 2 *K* and *L*). Harsher cleavage conditions (i.e., reducing the pH to 4.5, increasing the incubation time to 1 hr, and raising the incubation temperature to 20°C) were required to ablate UEA1 binding and the binding of the monoclonal blood group

H antibody to human surface mucous cells. These conditions also resulted in loss of cholera toxin B subunit binding and adherence of *H. pylori* strains WV229 and P466 (data not shown). Together, these results imply that *H. pylori* binding to UEA1-positive, fucosylated blood group antigen-positive, surface mucous cells in the human stomach is not dependent upon terminal nonsubstituted sialic acid residues. [α-L-Fucose-dependent adhesion to intestinal epithelial cells by *Campylobacter jejuni* and C. *coli* has been reported previously (33).] We cannot completely exclude involvement of a sialic acid in the postulated cell-associated adhesin receptor given the modest size of our lectin panel. However, the distribution of MAA and SNA lectin and cholera toxin B subunit binding sites plus the failure of fetuin and soluble sialyllactose to inhibit binding argue strongly against involvement of the α2,3-linked sialic acid residues that had been invoked in previous studies (8–10)—studies that employed cells that are not known targets for the organisms *in vivo*.

Perspectives. The *in situ* adherence assay described in this report should prove useful because it provides (*i*) a phenotypic parameter for characterizing clinical isolates of *H. pylori* and correlating their binding capacity with acid peptic disease and/or gastric neoplasia (e.g., compare the results obtained with WV229 and MO19), (*ii*) a way of characterizing structure/activity relationships in gastric (and intestinal) epithelial cell receptors for *H. pylori* adhesin(s), and (*iii*) a functional assay for identifying therapeutically useful compounds that inhibit strain- and cell lineage-specific binding of *H. pylori*.

The adherence assay suggests that binding of *H. pylori* strains is limited to surface mucous cells in the human gastric epithelium. This raises two obvious questions. (*i*) Given the rapid, upward, pipeline-like migration and perpetual exfoliation of these cells (14), how is this organism able to establish and maintain colonization of the stomach? (*ii*) What is the functional relationship, if any, between binding of *H. pylori* to surface mucous cells and the development of acid peptic disease and gastric neoplasia? Rapid cellular translocation and exfoliation of surface mucous cells represent a potential pathway for clearance of this organism. The inhibitory effect on bacterial binding of human colostrum secretory IgA is also of interest in this context, since it might be a natural scavenging mechanism that prevents colonization by this human pathogen at early stages of life. Our observation that *H. pylori* strains adhere to esophageal submucosal glands and glandular ducts raises the possibility that these habitats represent a "silent" colonization site for this bacterium, which may then seed the stomach. It is unclear at present how much molecular cross-talk exists between the components of this system. For example, does an inflammatory response triggered by binding of the adhesin (5) affect the cellular differentiation program of surface mucous cells so as to alter either cell migration rates, the integrity of junctional complexes between cells (34), the process of exfoliation, and/or the production of receptors for bacterial lectins? Alterations in surface mucous cells have been reported to be associated with *H. pylori* colonization: mucus content is reduced and binding of the sialic acid-specific lectin *Limax flavus* agglutinin is increased (35). Though little is known about the differentiation programs of gastric epithelial cell lineages, the *H. pylori* adhesin may represent an excellent probe for defining and perturbing these programs. Such an analysis may not only provide insights about the pathogenesis of acid peptic disease and cellular transformation associated with *H. pylori* infection, but may also help describe the role of its adhesin's receptor in regulating the biology of normal gastric epithelial cell populations.

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NOTES

Hemagglutination Activity of *Campylobacter pylori*

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Forty-five strains of *Campylobacter pylori* isolated from gastric biopsy specimens showed distinct hemagglutination activity. The activity was partially decreased by treatment with heat, trypsin, or an alkylating agent and was inhibited by porcine gastric mucin but not by various compounds, including D-mannose.

Campylobacter pylori, first isolated from human gastric mucosa in 1983 (19), is a microaerophilic S-shaped bacterium with flagella at one end. Evidence which suggests that the organism is an etiologic agent of human gastritis and possibly peptic ulcer is accumulating (2, 3, 6, 9, 10, 15, 18).

In biopsy specimens, *C. pylori* is found in the mucous layer and gastric pits (6, 14, 17) and is associated with gastric epithelial surfaces. Such close proximity to the mucosal surface must be important as the initial step in mucoidal colonization and infection by the bacterium, as is the case for many pathogenic bacteria (1). Ability of bacteria to attach to animal cells is usually assessed by hemagglutination. In this study we determined the hemagglutination activity of *C. pylori* as the first step to elucidate the relationship between this bacterium and pathogenesis of gastritis and peptic ulcer.

Strains of *C. pylori* were isolated from gastric biopsy specimens of patients undergoing upper gastrointestinal endoscopy at Yamaguchi University Hospital. Samples were taken from the site of pyloric glands, fundic glands, and the intermediary zone; homogenized in phosphate-buffered saline; incubated on sheep blood agar (Nissui) and on modified Skirrow medium (Nissui); and incubated at 37°C for 3 to 5 days under microaerophilic conditions (5% O_2, 10% CO_2, and 85% N_2). Curved gram-negative rods showing typical colony morphology of *C. pylori* were purified and given CPY (*Campylobacter pylori* culture collection of Yamaguchi University) numbers after identification on the basis of positive reactions for oxidase, catalase, urease; weak H_2S production; and negative reactions for nitrate reduction and hippurate hydrolysis. *C. pylori* NCTC 11637 isolated by B. Marshall (Royal Perth Hospital, Perth, Australia) was supplied by H. Inoue (Hyogo College of Medicine, Nishinomiya, Japan). Clinical isolates of *Campylobacter jejuni* and *Campylobacter coli* were provided by H. Tsuneoka (Nagato General Hospital, Nagato, Japan).

Bacteria were grown on triple-extract peptone agar (Eiken Chemical Co., Tokyo, Japan) supplemented with 6% sheep blood at 37°C for 2 to 3 days in a GasPak jar with an anaerobic gas generation kit (BBL Microbiology Systems, Cockeysville, Md.) without a catalyst. A 25-μl sample of bacterial suspensions which was titrated in twofold steps in phosphate-buffered saline was incubated with a 25-μl portion of a 0.25% erythrocyte suspension in 1% gelatin for 30 min at 37°C and stored at 4°C for 16 h. The endpoint was defined as the last dilution showing complete agglutination. Titers were expressed as reciprocals of endpoint dilutions. Titrations were carried out in duplicate, and the results were reproducible within one well.

Hemagglutination activity for human erythrocytes was determined with 45 strains of *C. pylori* and 18 strains of *C. jejuni* suspended in phosphate-buffered saline at a concentration of approximately 5×10^8 cells per ml. All the *C. pylori* strains tested had hemagglutination activity, and the hemagglutination titers were 1, 16, and 128 for the lowest, the average, and the highest values, respectively. On the other hand, only half of the *C. jejuni* strains showed slight hemagglutination, with the highest titer being 8. *C. pylori* NCTC 11637 and CPY0041-1 had hemagglutination titers of 128 and 16, respectively, and the latter was used for further studies. A strain of *C. coli* did not show hemagglutination. In addition to human erythrocytes, erythrocytes of other animals were agglutinated by the bacteria (Table 1).

Suspensions of CPY0041-1 (ca. 2×10^9 cells per ml, 250 μl) were incubated at various temperatures, and the remaining hemagglutination activity was determined (Table 2). The activity for guinea pig erythrocytes was stable at 37°C but inactivated rapidly at 56 and 100°C. The bacteria were also incubated with trypsin (type III; Sigma Chemical Co., St. Louis, Mo.) at 37°C and then incubated further for 10 min with trypsin inhibitor (type II-O; Sigma) (Table 2). The hemagglutination activity decreased rapidly but not com-

TABLE 1. Agglutination of erythrocytes from various animals by *C. pylori*

Source of erythrocytes	Hemagglutination titer
Mouse (fresh)	256
Rabbit (fresh)	32
Guinea pig (stored)	32
Human (fresh)	16
Human (stored)	16
Horse (stored)	8
Sheep (stored)	8

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TABLE 2. Effects of various treatments of *C. pylori* on guinea pig erythrocyte hemagglutination activity

Treatment	Time	Hemagglutination activity (%)
None		100
Heat (56°C)	5 min	25
	50 min	12.5
Heat (100°C)	5 min	12.5
	50 min	12.5
Trypsin (50 μg/ml)	5 min	50
	60 min	12.5
Trypsin (250 μg/ml)	5 min	6.3
	60 min	6.3
Formaldehyde (5%)	22 h	6.3

pletely. Essentially the same results were obtained for the agglutination of sheep erythrocytes.

To determine whether the heat-sensitive factors were also trypsin sensitive, bacteria were first treated with heat and then with trypsin. The hemagglutination titer to guinea pig erythrocytes decreased to 12.5% with incubation at 100°C for 30 min, and the titer decreased further to 6% after incubation with either 50, 250, or 500 μg of trypsin per ml. Alkylation of *C. pylori* with formaldehyde at 37°C also affected the hemagglutination activity (Table 2).

Previous studies have demonstrated that bacteria adhere to the surface of epithelial cells and that erythrocytes can be blocked by the compounds which mimic the receptors concerned (4, 5, 8, 11, 12, 16. 20). To detect specific inhibitors for *C. pylori* hemagglutination, the bacteria were preincubated with various compounds at 37°C for 30 min. None of the following compounds showed inhibitory effects on the agglutination of sheep and guinea pig erythrocytes: 250 mM D-mannose, 100 mM methyl-α-D-mannopyranoside, 100 mM L-fucose, 100 mM *N*-acetyl-D-galactosamine, 100 mM *N*-acetyl-D-glucosamine, 10 mM *p*-nitrophenyl-β-D-galactopyranoside, 1 mM *p*-nitrophenol, 1 mM 4-methylumbelliferone, 100 mM L-arginine, 100 mM L-serine, 5 mM $CaCl_2$, 5 mM EDTA, and 20 mg of bovine serum albumin per ml. In contrast, porcine gastric mucin (Nacalai Tesque Inc., Kyoto, Japan) showed a strong inhibitory effect, while bovine submaxillary mucin (type I-S; Sigma) showed a slight inhibition (Table 3). When the bacteria were heat treated, the residual activity was not affected by gastric or submaxillary mucin. These results suggest that gastric mucin has some role in the process of colonization by *C. pylori* on gastric epithelial-cell surfaces.

Neuraminidase treatment of erythrocytes is reported to abolish hemagglutination of certain strains of uropathogenic *Escherichia coli* (12). Incubation of sheep or guinea pig erythrocytes (10%, vol/vol) with *Clostridium perfringens* neuraminidase (5 U/ml; type V; Sigma) or trypsin (10 mg/ml) at 37°C for 60 min did not affect the hemagglutination activity of *C. pylori*.

TABLE 3. Inhibition of hemagglutination activity of *C. pylori* by porcine gastric and bovine submaxillary mucin

Mucin (mg/ml)	Hemagglutination activity (%) of:	
	Sheep erythrocytes	Guinea pig erythrocytes
None	100	100
Gastric (0.01)	50	50
Gastric (0.1)	12.5	25
Gastric (1.0)	6.3	ND[a]
Submaxillary (0.1)	100	50
Submaxillary (1.0)	25	50

[a] ND, Not determined because of hemolysis of guinea pig erythrocytes by gastric mucin.

The structure of the cells of *C. pylori* was examined by transmission electron microscopy after uranyl acetate staining and chromium shadowing. Several sheathed flagella (7) were seen at the end of the organism, but other filamentous structures such as pili or fimbriae were not observed. Therefore, a surface-associated molecule, possibly a protein, appears to be involved in the hemagglutination. Perez-Perez and Blaser showed common proteins in whole-cell and outer membrane preparations of *C. pylori* (13). Analysis of such proteins in relation to hemagglutination activity should be useful for characterization of adhesin molecules of *C. pylori*.

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described (24). The inner membrane potential was abolished with 25 μM carbonyl cyanide *p*-(trifluoromethoxy)phenylhydrazone (FCCP). Nonimported precursor was removed by digestion with proteinase K (200 μg per milliliter of import buffer) for 15 min at 4°C, followed by addition of 1 mM phenylmethylsulfonyl fluoride (PMSF). Proper insertion of radioactive precursors into the inner membrane was verified by checking resistance to extraction by 100 mM Na_2CO_3 (25) and resistance to proteinase K in mitoplasts (26).

14. For cross-linking, in vitro import was for 10 min at 20°C, and nonimported precursor was digested with proteinase K (30 μg/ml). Mitochondria were washed, resuspended at 1 mg/ml in import buffer, and incubated with 1 mM dithiobis(succinimidylpropionate) (DSP) for 30 min at 4°C followed by a quench with 100 mM tris-base, pH 8.0. For immunoprecipitation, solubilized mitochondria were incubated with monospecific polyclonal antibodies coupled to protein A–Sepharose (27).
15. For the multicopy suppressor screen, a yeast genomic DNA library in a 2μ,*URA3* vector was transformed into the temperature-sensitive yeast strains tim10-1 and tim12-1 (28). Transformants were grown at 25°C for 24 hours and then shifted to 37°C. Of 5×10^5 transformants in strain tim12-1, 300 transformants grew at 37°C. Subcloning of the genomic fragment carried by the suppressing plasmid S12 identified *TIM22* as the extragenic suppressor for the *tim12-1* mutation. Of 5×10^5 transformants in strain tim10-1, 46 transformants grew at 37°C; all of them contained only *TIM10* as the "suppressor" gene.
16. A hexahistidine tag was added to the COOH terminus of Tim10p by PCR amplification of *TIM10* with a primer that inserted six histidine codons immediately upstream of the stop codon. The PCR fragment was subcloned into YCplac111 (creating pTIM10H6) and then sequenced. Strain Tim10H6 was constructed by transformation of strain Δtim10[*TIM10*] with pTIM10H6 and subsequent removal of the plasmid carrying the wild-type *TIM10* gene on media containing 5-fluoro-orotic acid. To purify Tim10H6p and associated proteins, we solubilized mitochondrial protein (2 mg/ml) in 0.5% digitonin and 20 mM imidazole and incubated it with Ni^{2+}-nitrilotriacetic acid–Sepharose (Qiagen, Hilden, Germany). Polyclonal antibodies against Tim10p or Tim12p were raised against the recombinant proteins Tim10p that had been cleaved from a glutathione-S-transferase–Tim10p fusion or a thioredoxin-Tim12p fusion protein, respectively. Polyclonal antibodies against Tim22p were raised against a thioredoxin-Tim22p fusion protein in which the first 16 amino acids of Tim22p had been inserted between amino acids 34 and 35 of thioredoxin.
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Helicobacter pylori Adhesin Binding Fucosylated Histo-Blood Group Antigens Revealed by Retagging

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The bacterium *Helicobacter pylori* is the causative agent for peptic ulcer disease. Bacterial adherence to the human gastric epithelial lining is mediated by the fucosylated Lewis b (Le^b) histo-blood group antigen. The Le^b-binding adhesin, BabA, was purified by receptor activity–directed affinity tagging. The bacterial Le^b-binding phenotype was associated with the presence of the *cag* pathogenicity island among clinical isolates of *H. pylori*. A vaccine strategy based on the BabA adhesin might serve as a means to target the virulent type I strains of *H. pylori*.

Helicobacter pylori, a human-specific gastric pathogen, was first isolated in 1982 (*1*) and has emerged as the causative agent of chronic active gastritis and peptic ulcer disease (*2*). Most infected individuals show no clinical symptoms, implicating additional factors, such as genetic predisposition and the genotype of the infecting strain, in disease pathogenesis. Chronic infection is associated with the development of gastric adenocarcinoma, one of the most common types of cancer in humans (*3*), and *H. pylori* was recently defined as a class 1 carcinogen (*4*).

The bacterium colonizes the human gastric mucosa by adhering to the mucous epithelial cells and the mucus layer lining the gastric epithelium (*5*). These adherence properties protect the bacteria from the extreme acidity of the gastric lumen and displacement from the stomach by forces such as those generated by peristalsis and gastric emptying. The fucosylated blood group antigens Lewis b (Le^b) and H-1 (Fig. 1A) mediate adherence of *H. pylori* to human gastric epithelial cells in situ (*6*).

We have now biochemically characterized and identified the *H. pylori* blood group antigen–binding adhesin, BabA. Various strains of *H. pylori* were analyzed for binding to ^{125}I-labeled fucosylated blood group antigens (Fig. 1B) (*7*, *8*). Three of the five strains examined bound Le^b and H-1. The receptor specificities of these strains for the soluble blood group antigens correlate with their adherence properties in situ (*6*). The prevalence of blood group antigen–binding (BAB) activity was also assessed among 95 recent clinical isolates of *H. pylori*, and 66% (63 isolates) bound the Le^b antigen (*7*). None of the reference strains or the 95 recent isolates bound to the related Le^a, H-2, Le^X, or Le^Y antigens (Fig. 1, A and B). These results support previous observations of the receptor specificity of *H. pylori* for the Le^b and H-1 blood group antigens (*6*) and, in addition, demonstrate the high prevalence of BAB activity among clinical isolates.

Isolates of *H. pylori* are thought to differ in virulence and those from individuals with peptic ulcers most often are type I strains that express the vacuolating cytotoxin A (VacA) and the cytotoxin-associated gene A (CagA) protein (*9*). By definition, type II strains express neither marker. Twenty-one strains of previously defined type (*10*) and 73

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of the 95 recent isolates were analyzed for *cag* genotype (*11*) and binding to the Le^b antigen. The presence of *cagA* was associated with bacterial binding to the Le^b antigen; 73% (54/74) of $CagA^+$ strains, compared with 5% (1/20) of the $CagA^-$ strains, were positive for binding. The *cagA* gene is located in the 40-kb *cag* pathogenicity island (PAI), which contains genes that encode proteins with similarities to components of secretion systems (*12*). However, a deletion of the entire PAI that we engineered into a type I Le^b antigen–binding strain resulted in no reduction in Le^b antigen–binding activity (*13*). Thus, the epidemiological association between $CagA^+$ status and Le^b antigen–binding activity is not mechanistic.

We next determined the affinity constant (K_a) for the BabA-Le^b interaction by performing receptor displacement analyses (Fig. 1C). These results showed that the receptor-adhesin complex was formed under conditions of equilibrium. Most of the cells (>90%) of the bacterial population exhibited BAB activity, as determined with the use of confocal microscopy and fluorescent Le^b antigen (*14*). The K_a value for formation of the Le^b antigen–BabA complex was $\sim 1 \times 10^{10}\ M^{-1}$ (Fig. 1D) (*15*). The number of Le^b glycoconjugate molecules bound to BabA was calculated as ~500 per bacterial cell, similar to the number of fimbriae organelles on the surface of *Escherichia coli* (*16*).

The localization of BabA on the bacterial cell surface was investigated by immunogold electron microscopy. The BabA adhesin was detected on the bacterial cell outer membrane by probing with the Le^b antigen, but not with the Le^a antigen (Fig. 2, A and B) (*14*). No gold particles were located on the flagellar sheath, suggesting that, despite their continuity, the membranes of the cell surface and sheath differ in protein composition.

The molecular mass of the BabA protein was characterized by receptor overlay analysis. BAB activity corresponded to a single 75-kD band (Fig. 2C) (*17*); a 40-kD band also detected is probably endogenous peroxidase, possibly the 39-kD HP1461 peroxidase (*18*), because it stained without the Le^b conjugate overlay. The panel of strains from Sweden, Australia, and South America showed a conserved molecular mass of BabA (Fig. 2D).

Because the BabA protein is not abundant (Fig. 1D), we developed a combined ligand identification and purification technique, termed receptor activity–directed affinity tagging (ReTagging). Cross-linking agents with radiolabeled donative tags have previously been used for characterization of receptor ligands (*19*). However, for ReTagging, the Le^b glycoconjugate was equipped with an affinity tag–donating cross-linker structure. The modified Le^b glycoconjugate directed the targeted transfer of the affinity tag (biotin) to the BabA protein by virtue of its receptor activity (Fig. 3, A and B). After cross-linking, the covalently attached biotin tag was used to identify the adhesin with streptavidin (Fig. 2E) (*20*). One biotin-tagged protein of 75 kD was detected in several strains, consistent with the results of the overlay analysis (Fig. 2, C and D). More generally, ReTagging should prove useful for diverse studies of interactions whether in infectious disease, inflammation processes, or cell differentiation and development.

The high specificity of the ReTagging technique provided a means for affinity-purification of the adhesin protein. After cross-linking, bacteria were solubilized in SDS sample buffer, streptavidin-coated magnetic beads were added to the solubilized proteins, and biotin-tagged BabA protein was extracted (Fig. 3C) (*21*). The sequences of the 20 NH_2-terminal amino acids of the BabA ad-

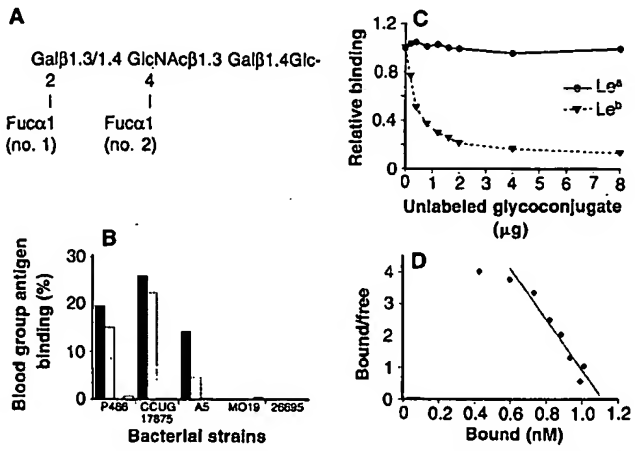

Fig. 1. Biochemical characterization of the blood group antigen–binding (BAB) activity of *H. pylori*. (**A**) The fucosylated blood group antigens. The H antigen (defining group O in the ABO blood group system) presents the Fucα1.2 residue (no. 1) in the core chain, the Le^a antigen instead presents the Fucα1.4 residue (no. 2), and the difucosylated Le^b antigen presents both fucose residues. The equivalent H-2, Le^X, and Le^Y antigens differ respectively by having a central β1.4 linkage, compared with the β1.3 linkage in the previous series (*30*). The fucosylated blood group antigens are typically found on red blood cells where they define the ABO blood group system, but they are also expressed on the epithelial cell surfaces as histo-blood group antigens (*30*). Gal, galactose; GlcNAc, *N*-acetylglucosamine; Glc, glucose. (**B**) Bacterial binding to soluble blood group antigens. Five *H. pylori* strains (*7*) were incubated with ^{125}I-labeled blood group antigen glycoconjugates (*8*). Solid bars, Le^b; open bars, H-1; striped (third) bars, Le^a; hatched (fourth) bars, H-2 plus Le^X plus Le^Y. (**C**) Receptor displacement assay. Strain CCUG17875 was incubated for 1 hour with 10 ng of ^{125}I-labeled Le^b conjugate, and the resulting complex was then challenged with an excess of unlabeled Le^b or Le^a conjugate. The remaining radioactivity in the bacterial pellet was measured (*8*). The Le^b conjugate, but not the Le^a conjugate, displaced the ^{125}I-labeled Le^b antigen from BabA. Concentrations of unlabeled conjugate ranged from 50 ng to 8 μg. (**D**) Scatchard analysis of the *H. pylori*–Le^b antigen interaction. Binding of strain CCUG 17875 to the Le^b antigen (*8*) was measured at Le^b conjugate concentrations of 10 to 260 ng/ml, yielding a K_a value of $8 \times 10^9\ M^{-1}$ (*15*).

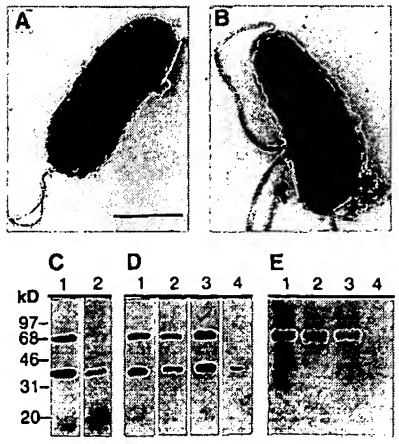

Fig. 2. Localization and characterization of the BabA adhesin. (**A** and **B**) Electron microscopy of cells of *H. pylori* strain CCUG17875 exposed to biotinylated Le^b or Le^a glycoconjugates, respectively. After washing, bacteria were incubated with 10-nm gold-labeled antibodies to biotin (ICN, Costa Mesa, California), counterstained, and air-dried onto formvar-coated copper grids (*14*). Bar, 1 μm. (**C**) Characterization of the molecular mass of the BabA adhesin by receptor overlay analysis (*17*). SDS-solubilized protein extracts of strain CCUG17875 were separated by SDS-PAGE and transferred to a PVDF membrane, which was then incubated with biotinylated Le^b glycoconjugate (lane 1) or biotinylated albumin (lane 2), followed by peroxidase-streptavidin. The positions of molecular size markers (in kilodaltons) are indicated on the left. (**D**) Receptor overlay analysis of BabA adhesins from various strains. Lanes 1 to 4: A5 (Sweden), P466 (South America), CCUG17875 (Australia), and MO19 (United States), respectively. The lack of a Le^b antigen–binding band with MO19 is consistent with this strain's lack of BAB activity (Fig. 1B). (**E**) Receptor activity–directed affinity tagging (ReTagging) (*20*) of BabA from various strains. Lanes are as in (D). Results are consistent with those in (D).

hesins from an Australian and a Swedish strain were found to be identical, and were used to construct degenerate polymerase chain reaction (PCR) primers for cloning purposes (*22*). Two sets of clones were identified that encode two proteins with almost identical NH_2-terminal domains and completely identical COOH-terminal domains (~300 amino acids), but with divergent central regions (Fig. 4A). For the identification of the functional *babA* gene, the BabA adhesin was subjected to large-scale purification by ReTagging, which provided sufficient protein for determination of the sequence of the 41 NH_2-terminal residues. The DNA sequence of one set of clones encoded this 41–amino acid sequence, and the corresponding gene was designated *babA*. The gene corresponding to the second set of clones was designated *babB*.

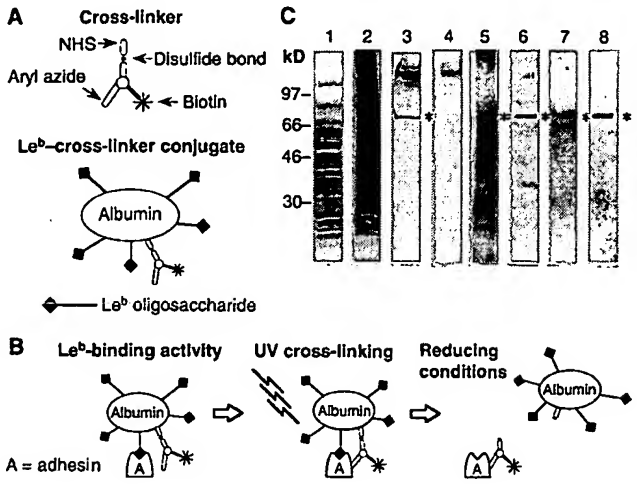

Fig. 3. ReTagging and purification of the BabA adhesin. **(A)** A multifunctional cross-linking agent was conjugated to the Le^b glycoconjugate. The Sulfo-SBED cross-linker contains an NHS group for conjugation to the protein core of the glycoconjugate, a central disulfide bond, a photoreactive aryl azide group, and a biotin side group (star) (*20*). **(B)** The cross-linker–labeled Le^b glycoconjugate is incubated with *H. pylori* so that binding to the bacteria brings the cross-linker molecule close to the adhesin protein. When the cells are subjected to ultraviolet (UV) irradiation, the photoreactive group forms a covalent bond to structures in the immediate vicinity (that is, the adhesin protein). Exposure to reducing conditions (DTT) results in cleavage of the disulfide bond in the cross-linker. The Le^b glycoconjugate is subsequently released and washed away. **(C)** Consecutive steps in the purification of BabA protein. Lane 1, SDS-PAGE and Coomassie blue staining of untreated bacterial protein extract (control). Lanes 2 and 3, protein extract after the ultraviolet-activated cross-linking reaction; lane 2 shows the Coomassie blue–stained gel and lane 3 shows blot detection of biotin-tagged proteins with peroxidase-streptavidin [the 75-kD BabA protein (asterisk) and some remaining Le^b glycoconjugate of >100 kD are apparent]. Lane 4, blot analysis of the protein extract after treatment with streptavidin-coated magnetic beads; no detectable biotin-tagged adhesin protein remained in the protein extract. Lanes 5 and 6, Coomassie blue–stained gel and blot analysis, respectively, of BabA protein eluted from the streptavidin-coated magnetic beads. Lanes 7 and 8, Coomassie blue–stained gel and blot analysis, respectively, of the protein preparation after final fractionation by preparative SDS-PAGE; BabA is now the dominant protein band (*21*). This band was excised for NH_2-terminal and COOH-terminal sequencing (*21, 23*).

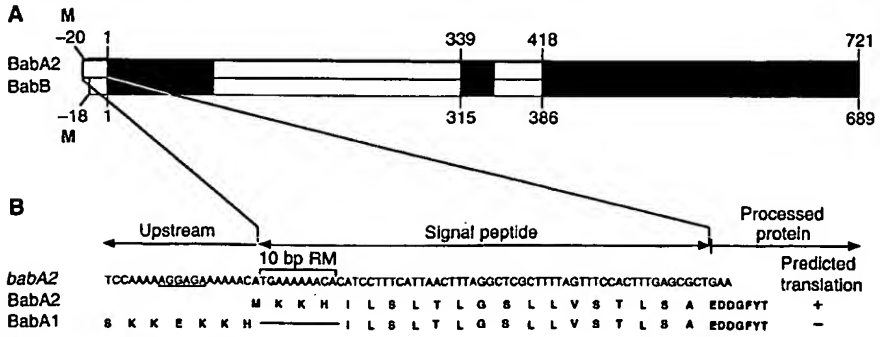

Fig. 4. (A) The translated *babA* and *babB* sequences showing regions of amino acid sequence similarity and heterogeneity in black and white, respectively. The BabA2 signal peptide starts at position −20. Position −18 of BabB indicates the predicted translational start position. Positions 721 for BabA (78 kD) and 689 for BabB (75 kD) indicate the ends of the open reading frames. **(B)** Nucleotide sequence of the upstream and signal peptide regions of the functional adhesin gene *babA2*. The putative Shine-Dalgarno sequence is underlined. The signal peptide sequences predicted by *babA1* and *babA2* are also shown. The 10-bp insert with a repeat motif (RM) is absent from *babA1*, which is otherwise identical to *babA2*, resulting in elimination of the start codon. A UAA termination codon is present at codon position −24 of the signal peptide region in *babA1*. The accession numbers for *babA1* and *babA2* are AF001388 and AF033654, respectively, with both predicted proteins being 91% identical to HP1243 (*18*). The accession number for *babB* is AF001389, with the predicted protein being 95% identical to HP896 (*18*). Abbreviations for the amino acid residues are: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.

The genes corresponding to both sets of clones appear to encode proteins with an 18- to 20-residue signal peptide sequence that would be cleaved during secretion to produce the determined NH_2-terminal EDD sequences. The calculated molecular size of the mature *babA* product is 78 kD (*23*). However, the cloned *babA* gene lacked an initiation codon at the start of the open reading frame (Fig. 4B). To localize additional *babA* gene alleles, we screened an ordered cosmid library, and two *babA* genes and one *babB* gene were mapped (*24*). Gene inactivation experiments identified the functional *babA* gene in strain CCUG17875, which expresses the BabA adhesin; inactivation of the second *babA* gene, now denoted *babA2*, resulted in a loss of Le^b antigen–binding activity, whereas inactivation of the original *babA* gene (*babA1*) did not affect Le^b antigen–binding activity (*24*). The functional *babA2* gene was subsequently amplified by PCR and sequenced (without cloning). The coding region was found to be identical to the previously cloned and sequenced *babA1* with the exception of an insert of 10 base pairs (bp) with a repeat motif in the signal peptide sequence, which resulted in the creation of a translational initiation codon (Fig. 4). Sequence analysis of the *babA2* gene obtained by PCR amplification and cloning in a plasmid in *E. coli* revealed frequent deletion of the repeat motif and convergence to the silent *babA1* gene, suggesting the presence of hot spots for phenotypic (phase) variation within the *bab* gene family (*25*).

The *babA* and *babB* coding sequences are highly similar to open reading frames in the sequenced genome of strain 26695 (open reading frames HP1243 and HP896, respectively) (*18*). The genomic location of *babA1* corresponds to that of open reading frame HP1243, as revealed by an almost perfect match between the upstream open reading frame HP1244 (ribosomal protein S18) and the sequence upstream of *babA1* from strain CCUG17875. No equivalent genomic location for the *babA2* upstream sequence was detected. Absence of the *babA2* allele might explain the lack of Le^b antigen–binding activity in strain 26695 (Fig. 1B). Although the *cag* PAI locus has a lower G+C content than the average of 39% for *H. pylori* (*18*), *babA* has a G+C content of 46%. Differences in G+C con-

tent may indicate the acquisition of genes and DNA loci from different sources.

The *bab* genes belong to a family of ~30 genes whose products show extensive amino acid sequence homology in the NH_2-terminal and COOH-terminal domains (*18*) (Fig. 4A), suggesting possibilities for recombination and consequent changes in the positions of individual genes. Evidence supporting this possibility is provided by the map positions of genes in several strains. In strain 26695, *babB* is located 5.3 kb from the *vacA* gene (*18*). Pulsed-field gel mapping also placed *babB* near *vacA* in strain NCTC11637 (*26*). In contrast, in strain NCTC11638 (*24*), *babA2* is located close to *vacA*. Recombination between duplicate segments would allow adhesin synthesis to be readily switched on or off. Such a mechanism might be important in determining host specificity during colonization and in bacterial persistence during chronic infection (*27*).

We propose that BabA-mediated adherence of *H. pylori* to gastric epithelium plays a critical role in efficient delivery of bacterial virulence factors that damage host tissue either directly or through inflammatory or autoimmune reactions, eventually leading to ulcer disease. Immunization experiments with adhesins of uropathogenic *E. coli* have demonstrated the potential for the generation of antibodies that inhibit adhesion (*28*). A vaccine strategy based on the BabA adhesin might possibly target the virulent type I strains of *H. pylori*, sparing the less virulent strains that may be constituents of the commensal flora (*29*).

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7. Strain CCUG17875 (Australia) was obtained from CCUG (Göteborg, Sweden). Strain A5, a gastric ulcer isolate, was from Astra Arcus (Södertälje, Sweden). Strains P466 (Peru), MO19 (United States), and NCTC11637 and -11638 were described previously (*6*). The genome of strain 26695 was recently sequenced (*18*). The panel of 95 *H. pylori* clinical isolates was obtained from the University Hospital in Uppsala, Sweden. Bacteria were grown at 37°C under 10% CO_2 and 5% O_2 (*6*) for 2 days to obtain optimal Le^b antigen–binding activity.
8. All blood group antigen glycoconjugates used were semisynthetic glycoproteins prepared by the conjugation of purified fucosylated oligosaccharides to human serum albumin (*6*) [P. D. Rye, *Nature Biotechnol.* **14**, 155 (1996)], and were from IsoSep AB (Tullinge, Sweden). The binding assay (Fig. 1B) was performed as previously described [P. Falk, T. Borén, D. Haslam, M. G. Caparon, *Methods Cell Biol.* **45**, 161 (1994)] with minor modifications. The H-1, Le^b, Le^a, H-2, Le^x, and Le^y glycoconjugates were labeled with ^{125}I by the chloramine T method. One milliliter of bacteria (optical density at 600 nm, 0.10) was incubated with 400 ng of ^{125}I-labeled conjugate (that is, an excess of receptor substrate) for 30 min in phosphate-buffered saline containing 0.5% albumin and 0.05% Tween-20. After centrifugation, the radioactivity bound to the bacterial pellet was measured with a gamma counter. Binding experiments were reproducible and performed in triplicate. In addition, the extent of BAB activity of each strain was stable.
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13. For the total *cag* PAI deletion, polymerase chain reaction (PCR) products from both ends of the *cag* PAI [generated with primers 2F and 4R (0.4 kb), and 24F and 25R (0.6 kb)] were cloned in pBluescript SK (Stratagene, La Jolla, CA). The *camR* gene [Y. Wang and D. E. Taylor, *Gene* **94**, 23 (1990)] was ligated between the fragments, and the product was used to transform *H. pylori* strain P119 (*31*). The *cag* PAI deletion status of the transformants was verified by their failure either to hybridize with any of several *cag* region probes or to yield PCR products with primers specific for internal regions of the *cag* PAI. The sequences of primers 2F and 4R, derived from cosmid 36 (*24*), and of 24F and 25R (*9*) are as follows: 2F, 5′-ACATTTTGGCTAAATAAACGCTG; 4R, 5′-TCTCCATGTTGCCATTATGCT; 24F, 5′-GGAATTATCACACCTTATAATGCCC; and 25R, 5′-TCATGCGAGCGGCGATGTG.
14. Confocal microscopy was performed with a Nikon/Multiprobe 2001 instrument (Molecular Dynamics, Sunnyvale, CA). Electron microscopy was performed with a JEOL 100 CX instrument.
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17. Cell extracts were solubilized in SDS sample buffer (without mercaptoethanol) at 37°C for 10 min and then subjected to SDS–polyacrylamide gel electrophoresis (SDS-PAGE). Proteins were then transferred to a polyvinylidene difluoride (PVDF) membrane. The membrane was incubated overnight with biotinylated Le^b glycoconjugate (1 μg/ml) or biotinylated albumin (negative control), prepared as previously described (*6*). After washing, the biotinylated structures bound by the BabA protein band were visualized with horseradish peroxidase–streptavidin and ECL reagents (Amersham).
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20. Bacteria were incubated with Le^b glycoconjugate to which the Sulfo-SBED cross-linker (Pierce, Rockville, IL) had been attached by *N*-hydroxysuccinimide ester (NHS). The photoreactive aryl azide cross-linker group was activated by ultraviolet irradiation. Bacteria were then washed with phosphate-buffered saline (pH 7.6) containing 0.05% Tween-20, protease inhibitors (EDTA and benzamidine), and 50 mM dithiothreitol (DTT). Bacterial proteins were separated by SDS-PAGE and transferred to a PVDF membrane, after which the biotin-tagged BabA protein was detected with peroxidase-streptavidin and ECL reagents (Fig. 2E).
21. Strains CCUG17875 and A5 were first processed by cross-linking and DTT treatment as described (*20*), and then solubilized in SDS sample buffer. The biotin-tagged BabA protein was then extracted with streptavidin-coated magnetic beads (Advanced Magnetics, Cambridge, MA). The beads were boiled in SDS sample buffer, and eluted proteins were alkylated. The protein preparation was further fractionated by preparative SDS-PAGE (Prep-Cell 491; Bio-Rad, Hercules, CA). The pooled BabA preparation was finally separated by SDS-PAGE and transferred to a PVDF membrane. The BabA band (15 pmol) was excised and the protein was subjected to NH_2-terminal sequencing (41 amino acids) with a Procise 494 instrument (Applied Biosystems, Foster City, CA). The biotin-tagged BabA adhesin was purified >3000-fold from the cell extract, and the yield was ~20%. The results of the Scatchard analysis (Fig. 1D) indicate that the level of BabA would be about five times higher compared to the resulting biotin-tagged BabA adhesin. The Retagging efficiency is dependent on the combined affinity and specificity in the receptor-ligand interaction and, in addition, the steric availability of the cross-linker structure. However, in our hands, a nonsaturated efficiency results in low background of unspecific biotin-tagging (Fig. 2E).
22. The NH_2-terminal sequence of BabA was used to design degenerate oligonucleotides for PCR amplification of a 59–bp fragment from the CCUG17875 chromosome. This 59-bp fragment was used to probe a low–copy number plasmid (pACYC184) library of CCUG17875 chromosomal DNA partially digested with Sau 3A.
23. The integrity and identity of the COOH-terminal domain was verified by COOH-terminal peptide sequencing. The BabA band (85 pmol) (*21*) was excised, and the last five amino acid residues were determined to be YV(F)A–, compared with YVFAY predicted from the gene sequence, with a Procise 494C instrument (Applied Biosystems). [(F), weak signal; –, amino acid not identified, probably because of derivatization during analysis]
24. An ordered cosmid library of strain NCTC11638 [N. O. Bukanov and D. E. Berg, *Mol. Microbiol.* **11**, 509 (1994)], in which *vacA* is located on cosmids 1 and 2, was probed with oligonucleotides for specific segments of the *babA* (A19) and *babB* (A18) genes. Whereas *babA* was mapped to the overlapping cosmids 43 and 44 (*babA1*) and to cosmids 1 and 2 (*babA2*), *babB* was mapped to cosmids 21 and 22. Thus, the *bab* gene locations perfectly match the RS1 (repetitive sequence 1) positions of the ordered cosmid library. Sequence analysis of strain CCUG 17875 revealed that *babA1* and *babA2* are identical in the coding region, with the exception of the 10-bp insert (Fig. 4). The sequences of primers A19 and A18 are 5′-GAAGAGGTGCTTTCTTGACCATTAG-CGTTACCCCCGCATTGCGT and 5′-CCATTTGC-GCTCTCGTTACTGCCAGGACCACAAGCAGTA-AA, respectively. For generation of the *babA* deletions, *babA*, including the *babA2* upstream sequence, was amplified with F2 (forward) and R39 (reverse) primers and cloned in pBluescript SK. The vector was linearized with primers R41 and F38. The *camR* gene (*13*) was ligated between the fragments, and strain CCUG17875 was transformed and subjected to selection for CamR. The transformants were analyzed for binding to ^{125}I-labeled Le^b glycoconjugate, and the location of the *camR* gene was analyzed by PCR with the upstream primers F2 (*babA2*) or F44 (*babA1*) in combination with primer R11. The sequences of the primers are as follows: F2, 5′-CTTAAATATCTCCCTATCCC; R39, 5′-CAAATACACGCTATAGAGCC; R41, 5′-GCGAGC-CTAAAGTTAATGA; F38, 5′-ACGTGGCGAACTTC-CAATTC; F44, 5′-CAGTCAAGCCCAAAGCTATGC; and R11, 5′-CGATTTGATAGCCTACGCTTGTG.
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26. Pulsed-field gel mapping was performed as described [Q. Jiang, K. Hiratsuka, D. E. Taylor, *Mol. Microbiol.* **20**, 833 (1996)]. The locations of the *babA* and *babB* genes were analyzed with PCR-generated probes. PCR was performed with the forward primers F43 (*babA*) or F15 (*babB*) in combination with primers R29 and R28, respectively. The sequences of the primers are as follows: F43, 5′-CTTGAG-CAAACTTTTGACCCGAT; F15, 5′-TGGGCCTATA-TCCACTGCAA; R29, 5′-AGTGCCAGCTGTTGA-TTTGTTGTTGCATGTGG; and R28, 5′-TACGCT-CACCCCCTTGCTCTTCATAACACA.
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31. We thank Q. Jiang and D. E. Taylor for analysis of the locations of the *babA* and *babB* genes; R. Gilman for *H. pylori* strain P119; K. A. Eaton for *H. pylori* strain 26695; P.-I. Ohlsson for NH_2-terminal sequencing; J. Van Beeumen and B. Samyn for COOH-terminal sequencing; R. Rosqvist for assistance with confocal microscopy; L. Johansson for assistance with electron microscopy; M. Block for image processing; R. Rappual for suggestions; Z. Xiang and S. Guidotti for strains; and D. L. Milton, J. Carlsson, B.-E. Uhlin, and P. Falk for critical reading of the manuscript. Supported by the Swedish Society of Medicine, Lion's Cancer Research Foundation, Umeå University, the Magnus Bergvall Foundation (T.B.), the Swedish Medical Research Council [grants 11218 (T.B.), 10848 (L.E.), and 7480 (L. Björck)], the Swedish Society for Medical Research (T.B. and D.I.), the Royal Swedish Academy of Sciences, the J. C. Kempe Memorial Foundation (D.I.), the Umeå University–Washington University Scientific Exchange Program (T.B. and J.Ö.), and grants from the NIH and American Cancer Society (D.E.B.) and from Chiron Co. (A.C.).

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Cancer Treatment by Targeted Drug Delivery to Tumor Vasculature in a Mouse Model

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In vivo selection of phage display libraries was used to isolate peptides that home specifically to tumor blood vessels. When coupled to the anticancer drug doxorubicin, two of these peptides—one containing an α_v integrin–binding Arg-Gly-Asp motif and the other an Asn-Gly-Arg motif—enhanced the efficacy of the drug against human breast cancer xenografts in nude mice and also reduced its toxicity. These results indicate that it may be possible to develop targeted chemotherapy strategies that are based on selective expression of receptors in tumor vasculature.

Endothelial cells in the angiogenic vessels within solid tumors express several proteins that are absent or barely detectable in established blood vessels (*1*), including α_v integrins (*2*) and receptors for certain angiogenic growth factors (*3*). We have applied in vivo selection of phage peptide libraries to identify peptides that home selectively to the vasculature of specific organs (*4*, *5*). The results of our studies imply that many tissues have vascular "addresses." To determine whether in vivo selection could be used to target tumor blood vessels, we injected phage peptide libraries into the circulation of nude mice bearing human breast carcinoma xenografts.

Recovery of phage from the tumors led to the identification of three main peptide motifs that targeted the phage into the tumors (*6*). One motif contained the sequence Arg-Gly-Asp (RGD) (*7*, *8*), embedded in a peptide structure that we have shown to bind selectively to $\alpha_v\beta_3$ and $\alpha_v\beta_5$ integrins (*9*). Phage carrying this motif, CDCRGDCFC (termed RGD-4C), homes to several tumor types (including carcinoma, sarcoma, and melanoma) in a highly selective manner, and homing is specifically inhibited by the cognate peptide (*10*).

A second peptide motif that accumulated in tumors was derived from a library with the general structure $CX_3CX_3CX_3C$ (X = variable residue, C = cysteine) (*6*). This peptide, CNGRCVSGCAGRC, contained the sequence Asn-Gly-Arg (NGR), which has been identified as a cell adhesion motif (*11*). We tested two other peptides that contain the NGR motif but are otherwise different from CNGRCVSGCAGRC: a linear peptide, NGRAHA (*11*), and a cyclic peptide, CVLNGRMEC. Tumor homing for all three peptides was independent of the tumor type and species; the phage homed to a human breast carcinoma (Fig. 1A), a human Kaposi's sarcoma, and a mouse melanoma (*12*). We synthesized the minimal cyclic NGR peptide from the CNGRCVSGCAGRC phage and found that this peptide (CNGRC), when coinjected with the phage, inhibited the accumulation of the CNGRCVSGCAGRC phage (Fig. 1A) and of the two other NGR-displaying phages in breast carcinoma xenografts (*12*).

The third motif—Gly-Ser-Leu (GSL) and its permutations—was frequently recovered from screenings using breast carcinoma (*6*), Kaposi's sarcoma, and malignant melanoma, and homing of the phage was inhibited by the cognate peptide (Fig. 1B). This motif was not studied further here.

The RGD-4C phage homes selectively to breast cancer xenografts (Fig. 1C). This homing can be inhibited by the free RGD-4C peptide (*10*), but not by the CNGRC peptide, even when this peptide was used in amounts 10 times those that inhibited the homing of the NGR phage (Fig. 1D). Tumor homing of the NGR phage was also partially inhibited by the RGD-4C peptide (Fig. 1E), but this peptide was only 10 to 20% as potent as CNGRC. An unrelated cyclic peptide, GACVFSIAHECGA, had no effect on the tumor-homing ability of either phage (*12*). Thus, our in vivo screenings yielded two peptide motifs, RGD-4C and NGR, both of which had previously been reported

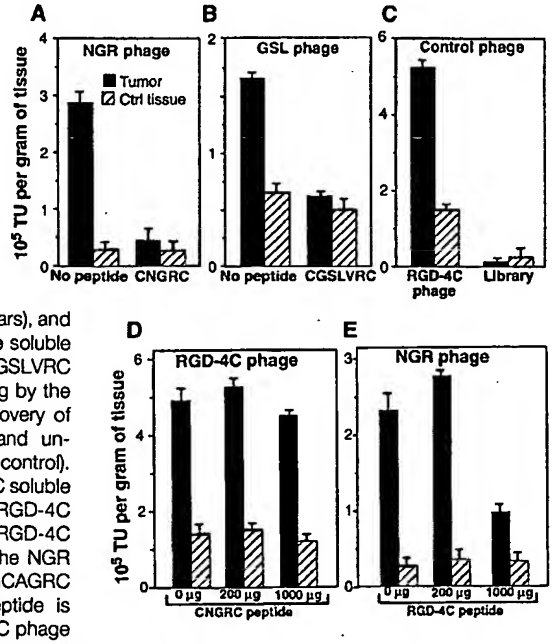

Fig. 1. Recovery of phage displaying tumor-homing peptides from breast carcinoma xenografts. Phage [10^9 transducing units (TU)] was injected into the tail vein of mice bearing size-matched MDA-MB-435–derived tumors (~1 cm^3) and recovered after perfusion. Mean values for phage recovered from the tumor or control tissue (brain) and the SEM from triplicate platings are shown. (**A**) Recovery of CNGRCVSGCAGRC phage from tumor (solid bars) and brain (striped bars), and inhibition of the tumor homing by the soluble peptide CNGRC. (**B**) Recovery of CGSLVRC phage and inhibition of tumor homing by the soluble peptide CGSLVRC. (**C**) Recovery of RGD-4C phage (positive control) and unselected phage library mix (negative control). (**D**) Increasing amounts of the CNGRC soluble peptide were injected with the RGD-4C phage. (**E**) Increasing amounts of the RGD-4C soluble peptide were injected with the NGR phage. Inhibition of the CNGRCVSGCAGRC phage homing by the CNGRC peptide is shown in (A); inhibition of the RGD-4C phage by the RGD-4C peptide has been reported (*10*).

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Search note 10/06 10:08

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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention t
the computation was performed at the SIB using the BLAST network serv
The SIB BLAST network service uses a server developed at SIB and the
BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller
Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein
database search programs. Nucleic Acids Res. 25:3389-3402(1997).

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Query: 20 AA
Date run: 2006-10-11 10:08:53 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.13 [Nov-27-2005]
Database: UniProtKB
3,494,645 sequences; 1,145,912,336 total letters
UniProt Knowledgebase Release 8.8 consists of:
UniProtKB/Swiss-Prot Release 50.8 of 03-Oct-2006: 234112 entries
UniProtKB/TrEMBL Release 33.8 of 03-Oct-2006: 3244331 entries

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to
Clustal W (multiple alignment) Submit Query
Select up to

☐ Include query sequence

	Db	AC	Description
☐	tr	O25840	_HELPY Outer membrane protein (Omp28) [HP_1243] [Helico.
☐	tr	O25556	_HELPY Outer membrane protein (Omp19) [HP_0896] [Helico.

- ☐ tr Q9ZKV2 _HELPJ Outer membrane protein-adhesin [babA] [Helicobac.
- ☐ tr O25086 _HELPY Outer membrane protein (Omp9) [HP_0317] [Helicob.
- ☐ tr Q1CUI5 _HELPH Outer membrane protein [HPAG1_0320] [Helicobacte.
- ☐ tr Q1CS19 _HELPH Outer membrane protein HopU [HPAG1_1186] [Helico.
- ☐ tr Q17SU1 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17ST6 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17ST8 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SW1 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SV3 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SU8 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SV9 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SV4 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SV7 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SV5 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ0 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17ST9 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SU0 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SY5 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SW4 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SW8 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17T02 _HELPY BabC (Fragment) [babC] [Helicobacter pylori (Cam.
- ☐ tr Q17SU2 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ1 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17T01 _HELPY BabC (Fragment) [babC] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ8 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SU6 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SW5 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SX3 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ9 _HELPY BabC (Fragment) [babC] [Helicobacter pylori (Cam.
- ☐ tr Q17SW2 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17ST7 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SY6 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SU5 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17SX2 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SZ5 _HELPY BabA (Fragment) [babA] [Helicobacter pylori (Cam.
- ☐ tr Q17SW7 _HELPY BabB (Fragment) [babB] [Helicobacter pylori (Cam.
- ☐ tr Q17T00 _HELPY BabC (Fragment) [babC] [Helicobacter pylori (Cam.
- ☐ tr Q1HW18 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q1HW20 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q1HW11 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q1HW09 _HELPY Adhesin-binding fucosylated histo-blood group an.
- ☐ tr Q1HW14 _HELPY Adhesin-binding fucosylated histo-blood group an.

Alignments

tr O25840 O25840_HELPY **Outer membrane protein (Omp28) [HP_1243] [Helicobacter pylori (Campylobacter pylori)]** 733 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

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Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr O25556 O25556_HELPY **Outer membrane protein (Omp19) [HP_0896] [Helicobacter pylori (Campylobacter pylori)]** 708 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

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Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 20 EDDGFYTSVGYQIGEAAQMV 39
```

tr Q9ZKV2 Q9ZKV2_HELPJ **Outer membrane protein-adhesin [babA] [Helicobacter pylori J99 (Campylobacter pylori J99)]** 744 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

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Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr O25086 O25086_HELPY **Outer membrane protein (Omp9) [HP_0317] [Helicobacter pylori (Campylobacter pylori)]** 745 AA align

Score = 68.1 bits (153), Expect = 4e-11
Identities = 20/20 (100%), Positives = 20/20 (100%)

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Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q1CUI5 Q1CUI5_HELPH **Outer membrane protein [HPAG1_0320] [Helicobacter pylori (strain HPAG1)]** 707 AA align

```
 Score = 68.1 bits (153), Expect = 4e-11
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 19 EDDGFYTSVGYQIGEAAQMV 38
```

tr Q1CS19 Q1CS19_HELPH **Outer membrane protein HopU [HPAG1_1186] [Helicobacter pylori (strain HPAG1)]** 738 AA align

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 Score = 68.1 bits (153), Expect = 4e-11
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 20 EDDGFYTSVGYQIGEAAQMV 39
```

tr Q17SU1 Q17SU1_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 247 AA align

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 Score = 68.1 bits (153), Expect = 4e-11
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 1  EDDGFYTSVGYQIGEAAQMV 20
          EDDGFYTSVGYQIGEAAQMV
Sbjct: 21 EDDGFYTSVGYQIGEAAQMV 40
```

tr Q17ST6 Q17ST6_HELPY **BabB (Fragment) [babB] [Helicobacter pylori (Campylobacter pylori)]** 243 AA align

Cell surface carbohydrates can also function as receptor molecules for a large number of bacteria, bacterial toxins, viruses, and protozoa (see, Sharon and Lis, Science, 246: 227-234 (1989); Karlsson, Ann. Rev. Biochem., 58: 309-350 (1989)).